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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 00:33:44 ; Search time 1026.35 seconds
(without alignments)
765.605 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27
Sequence: 1 aaacttcagtggtggacctccatgtt 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rnd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX281252	AX281252 Sequence
2	27	100.0	281	9	HSPSA4	X13943 Human PSA g
3	27	100.0	711	6	AR153342	AR153342 Sequence
4	27	100.0	711	6	BD007601	BD007601 Method fo
5	27	100.0	870	9	HSA459783	AJ459783 Homo sapi
6	27	100.0	876	9	HSA459782	AJ459782 Homo sapi
7	27	100.0	990	9	HSU17040	U17040 Human prost
8	27	100.0	992	6	I67863	I67863 Sequence 13
9	27	100.0	1130	9	AF335477	AF335477 Homo sapi
10	27	100.0	1350	6	AX200986	AX200986 Sequence
11	27	100.0	1350	6	AX267642	AX267642 Sequence
12	27	100.0	1415	9	HUMPA4	M21895 Human prost
13	27	100.0	1446	9	HUMAP3	M26663 Homo sapien
14	27	100.0	1462	6	I67864	I67864 Sequence 14
15	27	100.0	1466	6	E32812	E32812 Primer DNA
16	27	100.0	1466	9	HSPSA4	X05332 Human mRNA
17	27	100.0	1492	9	BC005307	BC005307 Homo sapi
18	27	100.0	1603	9	HSA310938	AJ310938 Homo sapi
19	27	100.0	1654	9	HUMPA4	M21896 Human prost
20	27	100.0	1729	6	AR059540	AR059540 Sequence
21	27	100.0	1729	6	AR082934	AR082934 Sequence
22	27	100.0	1729	6	AX337560	AX337560 Sequence
23	27	100.0	1729	9	HSPSA4	X07730 Human mRNA
24	27	100.0	1945	9	AF335478	AF335478 Homo sapi
25	27	100.0	2106	6	AX106218	AX106218 Sequence
26	27	100.0	3423	6	AX033404	AX033404 Sequence
27	27	100.0	3846	6	AX033402	AX033402 Sequence
28	27	100.0	4661	6	AX033400	AX033400 Sequence
29	27	100.0	4661	6	AX033401	AX033401 Sequence
30	27	100.0	5873	9	HSPSA4	X14810 Human DNA f
31	27	100.0	6153	9	HUMPSANTIG	M24543 Human prost
32	27	100.0	7130	6	A37262	A37262 Sequence 2
33	27	100.0	7130	6	AR167395	AR167395 Sequence
34	27	100.0	7130	9	HUMPSAA	M27274 Human prost
35	27	100.0	40458	9	AC011523	AC011523 Homo sapi
36	27	100.0	217346	2	AC027602	AC027602 Homo sapi
37	27	100.0	230000	9	AF243527	AF243527 Homo sapi
38	25.4	94.1	1514	9	MMPROS	X73560 M.mulatta m
39	21.2	78.5	146276	4	AC090889	AC090889 Canis fam
40	21	77.8	569	9	S75755	S75755 PSA=prostat
41	21	77.8	708	9	HSA310937	AJ310937 Homo sapi
42	20.6	76.3	95836	9	AC016710	AC016710 Homo sapi
43	20.6	76.3	146878	2	AC011174	AC011174 Homo sapi
44	20	74.1	20	6	I19503	I19503 Sequence 1
45	20	74.1	20	6	I67851	I67851 Sequence 1

ALIGNMENTS

RESULT 1	AX281252	AX281252	27 bp	DNA	linear	PAT 02-NOV-2001
AX281252	Sequence 9 from Patent WO0176622.					
LOCUS	AX281252					
DEFINITION	AX281252.1	GI:16608508				
ACCESSION	AX281252					
VERSION	AX281252.1					
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Pedyczak, A., Chong, P. and Sia, C.D.					
TITLE	Immunogenic peptides derived from prostate-specific antigen (psa)					
JOURNAL	and uses thereof					
	Patent: WO 0176622-A 9 18-OCT-2001;					

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FEATURES             Aventis Pasteur Limited (CA)
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                      /db_xref="taxon:32630"
                      /note="CLP316"
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Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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DB 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||

RESULT 2
HSPSA4              281 bp DNA linear PRI 24-FEB-1999
LOCUS               Human PSA gene for prostate specific antigen exon 4.
DEFINITION          X13943
ACCESSION           X13943.1 GI:35728
VERSION             kallikrein; prostate specific antigen; PSA gene.
KEYWORDS             Homo sapiens.
SOURCE              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM            Digby M.R.
REFERENCE            1 (bases 1 to 281)
AUTHORS             Direct Submission
TITLE               Submitted (09-JAN-1989) Digby M.R., The Howard Florey Institute,
JOURNAL             Melbourne University, Parkville, Victoria 3052, Australia
REFERENCE            2 (bases 1 to 281)
AUTHORS             Digby M., Zhang X.Y. and Richards R.I.
TITLE               Human prostate specific antigen (PSA) gene: structure and linkage
                    to the kallikrein-like gene, hK1-1
JOURNAL             Nucleic Acids Res. 17 (5), 2137 (1989)
MEDLINE             89183632
PUBMED              2467258
COMMENT             Data kindly reviewed (16-may-1989) by Digby M.R.
FEATURES            Location/Qualifiers
                      1..281
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                      /db_xref="taxon:9606"
                      /chromosome="19"
                      /clone="CHK-2"
                      /clone_lib="cosmid"
                      <1..52
                      /number=3
                      <53..>189
                      /note="prostate specific antigen"
                      /codon_start=3
                      /protein_id="CAA32126.1"
                      /db_xref="GI:1395283"
                      /db_xref="SWISS-PROT:P07288"
                      /translation="LTPKLCQVDLHVISNDVCAQVHPKVTKFMLCAGRWTKGKSTC
                      S"
                      53..189
                      /number=4
                      190..>281
                      /number=4
BASE COUNT          64 a 71 c 82 g 64 t
ORIGIN
Query Match          100.0%; Score 27; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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DB 67 AAACCTCAGTGTGGACCTCCATGTT 93
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RESULT 3
AR153342            711 bp DNA linear PAT 08-AUG-2001
LOCUS               Sequence 4 from patent US 6235486.
DEFINITION          AR153342
ACCESSION           AR153342.1 GI:15120874
VERSION             AR153342.1
KEYWORDS             Unknown.
SOURCE              Unknown.
ORGANISM            Unclassified.
REFERENCE            1 (bases 1 to 711)
AUTHORS             Young C.Y.F., Tindall D.J. and Klee G.G.
TITLE               Method for detection of breast cancer
JOURNAL             Patent: US 6235486-A 4 22-MAY-2001;
FEATURES            Location/Qualifiers
                      1..711
                      /organism="unknown"
BASE COUNT          148 a 208 c 206 g 149 t
ORIGIN
Query Match          100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
DB 436 AAACCTCAGTGTGGACCTCCATGTT 462
|||||

RESULT 4
BD007601            711 bp DNA linear PAT 31-JAN-2002
LOCUS               Method for detecting metastatic prostatic cancer.
DEFINITION          BD007601
ACCESSION           BD007601.1 GI:18635974
VERSION             JP 2001503991-A/14.
KEYWORDS             unidentified.
SOURCE              unidentified.
ORGANISM            unclassified.
REFERENCE            1 (bases 1 to 711)
AUTHORS             Tindall D.J., Young C.Y.F., McCormic D.J., Klee G.G., Saedi M.S.,
                    Kumar A., Rittenhouse H.G. and Wolfert R.L.
TITLE               Method for detecting metastatic prostatic cancer
JOURNAL             Patent: JP 2001503991-A 14 27-MAR-2001;
                    MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH, HYBRITECH INC
COMMENT             OS Unidentified
                    PN JP 2001503991-A/14
                    PD 27-MAR-2001
                    PF 14-NOV-1997 JP 1998522888
                    PR 14-NOV-1996 US 08/759354
                    PI DONALD J TINDALL, CHARLES Y F YOUNG, DANIEL J MCCORMIC, PI
                    GEORGE G KLEE,
                    PI MOHAMMAD, SAEED SAEDI, ABHAY KUMAR, HARRY G RITTENHOUSE, PI
                    ROBERT L WOLFERT
                    PC C12N15/09,C07K16/40,C12N5/10,C12N9/64,C12P21/08,C12Q1/68, PC
                    GOIN33/574,C12N15/00,C12N5/00
                    CC Strandedness: Double;
                    CC Topology: Linear;
                    FH Key
                    FT source
                    FT Location/Qualifiers
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                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT          148 a 208 c 206 g 149 t
ORIGIN
Query Match          100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.011;

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTTCAGTGTGGACCTCCATGTT 27
|||||
Db 436 AAACCTTCAGTGTGGACCTCCATGTT 462

RESULT 5
HSA459783
LOCUS
DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 2.
ACCESSION AJ459783
VERSION AJ459783.1 GI:20520642
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Heuze-Vourc'h, N. and Courty, Y.
TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 870)
AUTHORS Courty, Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabelais, 2 bis bvd Tonnelie, Tours, 37032 cedex, FRANCE
COMMENT alternative splice variant sequences: AJ459782, AJ459784.
FEATURES
source
1..870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="YC140405-00"
/tissue_type="prostate"
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/gene="KLK3"
CDS
22..807
/gene="KLK3"
/note="alternative splice variant 2"
/codon_start=1
/evidence="experimental"
/product="prostate specific antigen"
/protein_id="CAD30845.1"
/db_xref="GI:20520643"
/translation="MWPVVFVLTSTWIGAAPLILSRIVGGECEKHSQPVQLVAS RGRAVCGVLVHPQWVLTAAHCIRNKSIVLLGRHSFLPHDPTGVQVSHSFPHPLVD MSLLKNRFLRPGDSDSLDLRLSEPAELTDAVKVMDLPTQPALGTTCYASGWSI EPEEFTPKKLCQVDLHVISNDVCAQVHPKVTKEMLCAGRWGKSTCGSDSGGPLV CNGVLQGITSWGSEPCALPERPSLYTKVHYRWKIDTIIVANP"
22..72
/gene="KLK3"
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94..804
/gene="KLK3"
mat_peptide
/product="prostate specific antigen"
BASE COUNT 185 a 257 c 242 g 186 t
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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTTCAGTGTGGACCTCCATGTT 27
|||||
Db 529 AAACCTTCAGTGTGGACCTCCATGTT 555

RESULT 6
HSA459782
LOCUS
DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 1.
ACCESSION AJ459782
VERSION AJ459782.1 GI:20520640
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Heuze-Vourc'h, N. and Courty, Y.
TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 876)
AUTHORS Courty, Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabelais, 2 bis bvd Tonnelie, Tours, 37032 cedex, FRANCE
COMMENT alternative splice variant sequences: AJ459783, AJ459784.
FEATURES
source
1..876
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="YC171105-00"
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CDS
22..684
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/note="alternative splice variant 1"
/codon_start=1
/evidence="experimental"
/product="prostate specific antigen"
/protein_id="CAD30844.1"
/db_xref="GI:20520641"
/translation="MWPVVFVLTSTWIGAAPLILSRIVGGECEKHSQPVQLVAS RGRAVCGVLVHPQWVLTAAHCIRNKSIVLLGRHSFLPHDPTGVQVSHSFPHPLVD MSLLKNRFLRPGDSDSLDLRLSEPAELTDAVKVMDLPTQPALGTTCYASGWSI EPEEFTPKKLCQVDLHVISNDVCAQVHPKVTKEMLCAGRWGKSTCGSDSGGPLV WTGKSTCGSDSGGPLV CNGVLQGITSWGSEPCALPERPSLYTKVHYRWKIDTIIVANP"
22..72
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94..681
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mat_peptide
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BASE COUNT 220 a 235 c 231 g 190 c
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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTTCAGTGTGGACCTCCATGTT 27
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Db 406 AAACCTTCAGTGTGGACCTCCATGTT 432

RESULT 7
HSA17040
LOCUS
DEFINITION Human prostate specific antigen precursor mRNA, complete cds.
ACCESSION U17040
VERSION U17040.1 GI:595945
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 990)
AUTHORS Monne, M.M., Moreno, J.M., Mele, C.M., Mulholland, G.M. and Gomella, L.G.
TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence

JOURNAL Patent: WO 0173032-A 616 19-JUL-2001;
CORIXA CORPORATION (US)

FEATURES
Source Location/Qualifiers
1. .1350
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 284 a 404 c 391 g 271 t
ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGACCTCCATGTT 27
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Db 1129 AAATTCAGTGTGTGACCTCCATGTT 1155

RESULT 11
AX267642
LOCUS 1350 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 616 from Patent WO0173032.
ACCESSION AX267642
VERSION AX267642.1 GI:16516315
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
XU, J., DILLON, D.C., MITCHAM, J.L., HARLOCKER, S.L., JIANG, Y.,
KALOS, M.D., FANGER, G.R., RETTER, M.W., STOLK, J.A., DAY, C.H.,
VEDWICK, T.S., CARTER, D., LI, S.X., WANG, A., SKEIKY, Y.A., HEPLER, W.T.
and HENDERSON, R.A.
TITLES Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0173032-A 616 04-OCT-2001;

CORIXA CORPORATION (US)
FEATURES
Source Location/Qualifiers
1. .1350
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/db_xref="taxon:9606"

BASE COUNT 284 a 404 c 391 g 271 t
ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGACCTCCATGTT 27
|||||
Db 1129 AAATTCAGTGTGTGACCTCCATGTT 1155

RESULT 12
HUMPA
LOCUS 1415 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human prostate specific antigen (PA) gene, 3 end, clone PA 75.
ACCESSION M21895
VERSION M21895.1 GI:189523
KEYWORDS glycoprotein; prostate antigen; prostate-specific antigen;
seminogelin.

SOURCE Human prostate tumor cell line PC 82, cDNA to mRNA, clone PA 75.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1415)
Riegmann, P.H., Klaassen, P., van der Korp, J.A., Romijn, J.C. and
Trapman, J.

TITLES Molecular cloning and characterization of novel prostate antigen
cDNA's

JOURNAL Biochem. Biophys. Res. Commun. 155 (1), 181-188 (1988)
MEDLINE 88326297

PUBMED 2458104
FEATURES
Source Location/Qualifiers
1. .1415
/organism="Homo sapiens"
/db_xref="taxon:9606"

gene
1. .1415
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CDS
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/note="prostate specific antigen precursor"
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/db_xref="GI:189524"

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VCGGVLPWVOWVLTAAHCIRKNSVILLGRHSLEFHPEDTGOVQVSHSPHPLXMSLL
KNRFLRPGDSSHDLMLRLSEPAELTDAKRVMDLPTQEPALGTTCYASGWSIEPPEE
FLTPKRLQCVDLHVISNDVCAQVHPKVKFMLCAGRWTKGKSTCGSDSGGGLVNCNGV
LQGITTSWGSEPCALPSPSLYTKVVHYRWIKDTIVANP"

<1. .40
/gene="APS"

/note="prostate specific antigen signal peptide"

62. .772
/gene="APS"

/product="prostate specific antigen"

BASE COUNT 328 a 361 c 410 g 316 t
ORIGIN 176 bp upstream of PvuII site.

Query Match 100.0%; Score 27; DB 9; Length 1415;

Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGACCTCCATGTT 27
|||||
Db 497 AAATTCAGTGTGTGACCTCCATGTT 523

RESULT 13

HUMAPS

LOCUS 1446 bp mRNA linear PRI 04-JAN-1995

DEFINITION Homo sapiens prostate-specific antigen mRNA, complete cds.

ACCESSION M26663

VERSION M26663.1 GI:618463

KEYWORDS prostate-specific antigen.

SOURCE Homo sapiens prostate gland cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Henttu, P. and Viikko, P.

TITLE cDNA coding for the entire human prostate specific antigen shows

high homologies to the human tissue kallikrein genes

JOURNAL Biochem. Biophys. Res. Commun. 160 (2), 903-910 (1989)

MEDLINE 89246551

PUBMED 2470373

COMMENT On Jan 5, 1995 this sequence version replaced gi:341511.

Ref [1] reports bases 1-135 only.

FEATURES
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/map="19q13.3"

/clone="PSA-20"

/tissue_type="prostate gland"

1. .1446
/gene="APS"

1. .24
/gene="APS"

/note="G00-119-695"

25. .810
/gene="APS"

/note="AA 18. .24 propeptide; AA 69 glycosylated Asn

residue"
/codon_start=1
/product="prostate-specific antigen"
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/db_xref="GI:618464"
/db_xref="GDB:G00-119-695"

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RGRACGVLVHPQSVLTAAHCRNKSIVLLGRHSFLHPEDTGOVQVSHSPHPLVD
MSLKNRFLRGDSSDLMLRLSEPAELTDAVKVMDLPTQEPALGTTTCVASGWSI
EPFELTKLQCVDLHVISNDCAOVHPQKTKMLCAGRTGKSTCGSDSGGLV
CNGVLOGITSGSEPCALPERPSLYKVVHYRWKIDTIVNP"

sig_peptide

/gene="APS"
/note="G00-119-695"

mat_peptide

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/product="prostate-specific antigen"

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811..1446
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3'UTR

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polyA_site

1446
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BASE COUNT

333 a 372 c 419 g 322 t

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Query Match 100.0%; Score 27; DB 9; Length 1446;

Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTCAGTGTGTGGACCTCCATGTT 27

Db 532 AAACCTCAGTGTGTGGACCTCCATGTT 558

RESULT 14

I67864

LOCUS 167864 1462 bp DNA linear PAT 04-FEB-1998

DEFINITION Sequence 14 from patent US 5674682.

ACCESSION 167864

VERSION 167864.1 GI:2829986

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1462)

AUTHORS Croce,C., Gomella,L., Mulholland,S.,Grant., Moreno,J.G. and

Fischer,R.

TITLE Nucleic acid primers for detecting micrometastasis of prostate

JOURNAL Cancer

PATENT: US 5674682-A 14 OCT-1997;

FEATURES

Location/Qualifiers

1..1462

/organism="unknown"

BASE COUNT 343 a 374 c 422 g 323 t

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1462;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTCAGTGTGTGGACCTCCATGTT 27

Db 532 AAACCTCAGTGTGTGGACCTCCATGTT 558

RESULT 15

E32812

LOCUS 1466 bp RNA linear PAT 31-JAN-2002

DEFINITION Primer DNA and method for detecting mRNA encoding prostate

gland-specific antigen by using the same.

ACCESION E32812

VERSION E32812.1 GI:18623942

KEYWORDS JP 2000069969-A/5.

SOURCE unclassified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1466)

AUTHORS Nakagawa,H.

TITLE Primer DNA and method for detecting mRNA encoding prostate

gland-specific antigen by using the same

JOURNAL Patent: JP 2000069969-A 5 07-MAR-2000;

COMMENT HITACHI CHEMICAL CO LTD,KK NIHON IDENSHI KENKYUJO

OS Unidentified

PN JP 2000069969-A/5

PD 07-MAR-2000

PF 28-AUG-1998 JP 1998243419

PR HIROKAZU NAKAGAWARA

PC C12N15/09,C12Q1/68,C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

PH Key Location/Qualifiers

FT source 1..1466

/organism="Unidentified"

FEATURES

Location/Qualifiers

1..1466

/organism="Unidentified"

/db_xref="taxon:32644"

BASE COUNT 338 a 382 c 422 g 324 t

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1466;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAACCTCAGTGTGTGGACCTCCATGTT 27

Db 551 AAACCTCAGTGTGTGGACCTCCATGTT 577

Search completed: November 19, 2002, 04:02:55

Job time : 1028.68 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 ; Search time 1542.46 seconds
(without alignments)
283.494 Million cell updates/sec

Title: US-09-829-004a-9

Perfect score: 27

Sequence: 1 aaactcagtggtgacccatggt 27

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	189	9	AA657663 nt82c06.s
2	27	100.0	196	12	BF588362
3	27	100.0	239	12	BF588359
4	27	100.0	241	12	BE769440
5	27	100.0	272	14	T29518
6	27	100.0	288	12	BF588848

C 7	27	100.0	310	9	AA522842
C 8	27	100.0	319	12	BF56613
C 9	27	100.0	328	9	AA654296
C 10	27	100.0	329	12	BF588271
C 11	27	100.0	351	12	BE838775
C 12	27	100.0	354	12	BE771925
C 13	27	100.0	373	9	AA228853
C 14	27	100.0	388	9	AA228822
C 15	27	100.0	398	9	AA635287
C 16	27	100.0	400	12	BF476990
C 17	27	100.0	406	9	AA420570
C 18	27	100.0	420	9	AA228836
C 19	27	100.0	426	9	AA226359
C 20	27	100.0	429	12	BF56615
C 21	27	100.0	429	12	BF56642
C 22	27	100.0	436	9	AA630877
C 23	27	100.0	439	9	AA569482
C 24	27	100.0	453	9	AA573727
C 25	27	100.0	454	12	BE769339
C 26	27	100.0	457	9	AI926979
C 27	27	100.0	466	9	AA654527
C 28	27	100.0	471	9	AA654924
C 29	27	100.0	481	9	AA579159
C 30	27	100.0	489	9	AA658261
C 31	27	100.0	491	9	AA225115
C 32	27	100.0	505	9	AA574023
C 33	27	100.0	514	9	AI989309
C 34	27	100.0	520	9	AA534235
C 35	27	100.0	520	12	BF56617
C 36	27	100.0	540	12	BF56640
C 37	27	100.0	542	9	AA654548
C 38	27	100.0	554	9	AA579039
C 39	27	100.0	582	9	AA594946
C 40	27	100.0	591	12	BF679591
C 41	27	100.0	636	12	BF678378
C 42	27	100.0	681	9	AI732097
C 43	27	100.0	724	12	BF964653
C 44	27	100.0	732	9	AI547309
C 45	27	100.0	738	12	BF679168

ALIGNMENTS

RESULT 1
AA657663
LOCUS
DEFINITION
AA657663
ACCESSTION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA657663 189 bp mRNA linear EST 05-NOV-1997
nt82c06.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1205002
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN).
mRNA sequence.

AA657663
AA657663.1 GI:2593817
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd ET from Amerisham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .189
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1205002"
/clone_lib="NCI_CGAP_P3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

/note="Vector: pAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors. 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the ligation cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT

43 a 44 c 54 g 48 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAATTCAGTGTGGACCTCCATGTT 27

Db 10 AAATTCAGTGTGGACCTCCATGTT 36

RESULT 2

BF858362

LOCUS

RC5-FT0193-211100-012-G09_1 FT0193 Homo sapiens cDNA, mRNA EST 16-JAN-2001

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 196)

REFERENCE

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE

JOURNAL

MEDLINE

COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-
211100-012-G09.1&t3=2000-11-21&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 190.

FEATURES

Location/Qualifiers

source

1. .196
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FT0193"
/dev_stage="Adult"

/note="Organ: prostate_tumor; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

41 a 58 c 55 g 42 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 196;

Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAATTCAGTGTGGACCTCCATGTT 27

Db 146 AAATTCAGTGTGGACCTCCATGTT 172

RESULT 3

BF858359/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

ORGANISM

REFERENCE

AUTHORS

ORGANISM

REFERENCE

AUTHORS

ORGANISM

REFERENCE

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REFERENCE

BASE COUNT 52 a 67 c 70 g 50 t
ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
|||||
Db 94 AAATTCAGTGTGTGGACCTCCATGTT 68

RESULT 4

BE769440

LOCUS

DEFINITION PM1-FT0028-030700-001-c02_1 FT0028 Homo sapiens cDNA, mRNA EST 20-SEP-2000

ACCESSION

BE769440

VERSION

BE769440.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=ft2-pm1-FT0028-030

700-001-c02-1&t3=2000-07-03&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 241.

FEATURES

source

1. .241

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="FT0028"

/dev_stage="Adult"

/notes="Organ: prostate_tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 51 a 71 c 68 g 51 t

ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 241;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27

|||||

Db 146 AAATTCAGTGTGTGGACCTCCATGTT 172

RESULT 5

T29518

LOCUS

DEFINITION

T29518

ACCESSION

T29518

VERSION

T29518.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Adams, M.D., Kerlavage, A. R., Fleischmann, R. D., Fullner, R. A., Bult

C. J., Lee, N., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White

O., Sutton, G., Blake, J. A., Brandon, R. C., Chiu, M. W., Clayton, R. A.,

Cline, R. T., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald

L. M., FitzHugh, W. M., Fritchman, J. L., Geoghegan, N. S. M., Glodok, A.,

Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, J. P. S., Kelley, J. M.,

Klimek, K. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M.,

Moreno-Palauques, R. F., McDonald, L. A., Nguyen, D. T., Pellegrino, S. M.,

Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R.,

Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. P., Li, Y.,

Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,

Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G. A., He, W. W.,

Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A., Kozak, D. L.,

Kunsch, C., Ji, H., Li, H., Weissner, P. S., Olsen, H., Raymond, L., Wei

Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon

M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and

Venter, J. C.

TITLE

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

JOURNAL

MEDLINE

COMMENT

Contact: Venter, J. C.

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org)

Seq primer: M13 Reverse.

FEATURES

source

1. .272

/organism="Homo sapiens"

/db_xref="ATCC (inhost):106527"

/db_xref="taxon:9606"

/clone_lib="Human prostate gland"

/note="Organ: prostate gland"

BASE COUNT 62 a 81 c 71 g 56 t 2 others

ORIGIN

Query Match 100.0%; Score 27; DB 14; Length 272;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27

|||||

Db 190 AAATTCAGTGTGTGGACCTCCATGTT 216

RESULT 6

BF588848/c

LOCUS

DEFINITION

BF588848

7112c03.x1 NCI_CGAP Br16 Homo sapiens cDNA clone IMAGE:3334468 3'

similar to SW:PROS_HUMAN P07288 PROSTATE SPECIFIC ANTIGEN PRECURSOR

,, mRNA sequence.

ACCESSION

BF588848

VERSION

BF588848.1

KEYWORDS

EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 288)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@rcmail.nih.gov
Tissue Procurement: Dennis Sgroi, M.D., Kristina Cole, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..288
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:334458"
/clone_lib="NCI-CCGAP-Br16"
/sex="female"
/tissue_type="lobular carcinoma in situ"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: breast; Vector: PAMPI; mRNA made from breast
carcinoma tissue, cDNA made by oligo-dr priming.
Directionally cloned. Size selected on agarose gel,
average insert size 400 bp. Primary library,
non-amplified."
59 a 83 c 87 g 59 t

BASE COUNT
ORIGIN
Query Match 100.0%; Score 27; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
DB 119 AAACCTCAGTGTGGACCTCCATGTT 93

RESULT 7
AA522842/c
LOCUS
DEFINITION
ni72c08.s1 NCI-CCGAP-Pr12 Homo sapiens cDNA clone IMAGE:982382
similar to gp:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN).
mRNA sequence.
AA522842
VERSION
KEYWORDS
SOURCE
EST.
GI:2263554
human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 310)
AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@rcmail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuquil, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 426 Std Error: 0.00
Seq primer: -40ml3 fwd, ET from Amersham.
Location/Qualifiers
1..310
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:982382"
/clone_lib="NCI-CCGAP-Pr12"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/note="Vector: PAMPI0; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dr priming.
Non-directionally cloned. Size selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."
72 a 82 c 62 g 94 t

BASE COUNT
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
DB 302 AAACCTCAGTGTGGACCTCCATGTT 276

RESULT 8
BF856613/c
LOCUS
DEFINITION
BP856613
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:12244370
human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 319)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICP Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=HRI&t2=MRI-FT0200-311000-001-bll&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 269.
Location/Qualifiers
1..319
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FT0200"
/dev_stage="Adult"
/note="Organ: prostate_tumor; Vector: puc18; Site: 1; SmaI;

Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 64 a 84 c 95 g 76 t
ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0;

QY 1 AAATTCAGTGTGGACCTCCATGTT 27
|||||
Db 66 AAATTCAGTGTGGACCTCCATGTT 40

RESULT 9
AA654296
LOCUS
DEFINITION
AA654296 328 bp mRNA linear EST 04-NOV-1997
nt83c06 s1 NCI-CGAP Pr3 Homo sapiens cDNA clone IMAGE:1205098
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN
); contains MSRI.b2 MSRI repetitive element 1, mRNA sequence.
AA654296
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 328)

AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 298.

FEATURES
source
1..328
Location/Qualifiers
/organism="Homo sapiens",
/db_xref="taxon:9606"
/clone="IMAGE:1205098"
/clone_lib="NCI-CGAP_Pr3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDG-cloning method (Life technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
BASE COUNT 66 a 76 c 113 g 73 t
ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATTCAGTGTGGACCTCCATGTT 27
|||||
Db 150 AAATTCAGTGTGGACCTCCATGTT 176

RESULT 10
BF858271/c
LOCUS
DEFINITION
RC5-FT0193-201100-012-H06 FT0193 Homo sapiens cDNA, mRNA sequence.
BF858271
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 329)
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordino, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
COMMENT
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC56t2-RC5-FT0193-
201100-012-H06&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 48
High quality sequence stop: 329.
FEATURES
Location/Qualifiers
1..329
/organism="Homo sapiens",
/db_xref="taxon:9606"
/clone_lib="FT0193"
/dev_stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 68 a 99 c 96 g 66 t
ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGGACCTCCATGTT 27
|||||
Db 184 AAATTCAGTGTGGACCTCCATGTT 158

RESULT 11
BE838775
LOCUS
DEFINITION
RC6-FN0114-090800-011-F04 FN0114 Homo sapiens cDNA, mRNA sequence.
BE838775 351 bp mRNA linear EST 22-SEP-2000

BE838775
 VERSION BE838775.1 GI:10271153
 EST.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 351)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bucher, P., Jongeneel, C.V., O'Hare
 Brunstein, A., deOliveira, P.S., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-FN0114-090
 800-011-F04&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 278.
 Location/Qualifiers
 1..351
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0114"
 /dev_stage="Adult"
 /note="Organ: prostate_tumor; Vector: puc18; Site: 1; SmaI
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 79 a 97 c 97 g 77 t 1 others
 BASE COUNT 79 a 97 c 97 g 77 t 1 others
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 27; DB 12; Length 351;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAACCTCAGTGTGACCTCCATGTT 27
 Db 53 AAACCTCAGTGTGACCTCCATGTT 79
 RESULT 12
 BE771925
 LOCUS BE771925
 DEFINITION CM3-F70097-300600-225-c11 F70097 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BE771925
 VERSION BE771925.1 GI:10225583
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bucher, P., Jongeneel, C.V., O'Hare
 Brunstein, A., deOliveira, P.S., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-FN0114-090
 800-011-F04&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 278.
 Location/Qualifiers
 1..351
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0114"
 /dev_stage="Adult"
 /note="Organ: prostate_tumor; Vector: puc18; Site: 1; SmaI
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 79 a 97 c 97 g 77 t 1 others
 BASE COUNT 79 a 97 c 97 g 77 t 1 others
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 27; DB 12; Length 351;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAACCTCAGTGTGACCTCCATGTT 27
 Db 53 AAACCTCAGTGTGACCTCCATGTT 79
 RESULT 12
 BE771925
 LOCUS BE771925
 DEFINITION CM3-F70097-300600-225-c11 F70097 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BE771925
 VERSION BE771925.1 GI:10225583
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bucher, P., Jongeneel, C.V., O'Hare
 Brunstein, A., deOliveira, P.S., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
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 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-FN0114-090
 800-011-F04&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 278.
 Location/Qualifiers
 1..354
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0097"
 /dev_stage="Adult"
 /note="Organ: prostate_tumor; Vector: puc18; Site: 1; SmaI
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 81 a 98 c 99 g 76 t
 BASE COUNT 81 a 98 c 99 g 76 t
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 27; DB 12; Length 354;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAACCTCAGTGTGACCTCCATGTT 27
 Db 65 AAACCTCAGTGTGACCTCCATGTT 91
 RESULT 13
 AA228953
 LOCUS AA228953
 DEFINITION ncl4a04.r1 NCI_CGAP_Prl Homo sapiens CDNA clone IMAGE:1008078
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);;
 mRNA sequence.
 AA228953
 AA228953.1 GI:1851772
 EST.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 373)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Copied to: Robert Strausberg, Ph.D.
 Email: rgabbs-remail.nih.gov
 Tissue procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
 Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 Simpson, A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-F70097-300
 800-011-F04&t3=2000-06-30&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 25
 High quality sequence stop: 354.
 Location/Qualifiers
 1..354
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0097"
 /dev_stage="Adult"
 /note="Organ: prostate_tumor; Vector: puc18; Site: 1; SmaI
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 81 a 98 c 99 g 76 t
 BASE COUNT 81 a 98 c 99 g 76 t
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 27; DB 12; Length 354;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAACCTCAGTGTGACCTCCATGTT 27
 Db 65 AAACCTCAGTGTGACCTCCATGTT 91
 RESULT 13
 AA228953
 LOCUS AA228953
 DEFINITION ncl4a04.r1 NCI_CGAP_Prl Homo sapiens CDNA clone IMAGE:1008078
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);;
 mRNA sequence.
 AA228953
 AA228953.1 GI:1851772
 EST.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 373)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Copied to: Robert Strausberg, Ph.D.
 Email: rgabbs-remail.nih.gov
 Tissue procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
 Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 342.

FEATURES

source

Location/Qualifiers
1. .373
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Prl"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

/note="Vector: pAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10 ,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 78 a 106 c 107 g 82 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 373;

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTTCAGTGTGTGGACCTCCATGTT 27

Db 203 AAATTTCAGTGTGTGGACCTCCATGTT 229

RESULT 14

AA228822/c

LOCUS

DEFINITION AA228822 388 bp mRNA linear EST 20-AUG-1997
nc15a04.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008174
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION

AA228822

VERSION

AA228822.1

GI:1851679

KEYWORDS

EST.

SOURCE

HUMAN.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 388)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

, Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 648 Std Error: 0.00

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 341.

FEATURES

source

Location/Qualifiers
1. .388
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Prl"

/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

/note="Vector: pAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10 ,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 81 a 119 c 102 g 86 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 388;

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTTCAGTGTGTGGACCTCCATGTT 27

Db 314 AAATTTCAGTGTGTGGACCTCCATGTT 288

RESULT 15

AA635287

LOCUS

DEFINITION AA635287 398 bp mRNA linear EST 03-DEC-1997
nt71b07.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1203925
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION

AA635287

VERSION

AA635287.1

GI:2619092

KEYWORDS

EST.

SOURCE

HUMAN.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 398)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

On Nov 12, 1997 this sequence version replaced gi:2559129.

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

, Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 651 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .398
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Pr3"

/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

/note="Vector: pAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of

DNase-treated, total cellular RNA obtained from 5,000-10 ,000 microdissected cells histologically-determined to be

fully malignant prostate cancer cells. Double-stranded

cDNA was ligated to EcoRI adaptors, 5 cycles of PCR

applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDC-cloning method (Life Technologies). Average insert size is 500 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

**BASE COUNT
ORIGIN**

88 a	106 c	116 g	88 t.

Query Match
100.0%; Score 27; DB 9; Length 398;

Query Match 100.0%; Score 27; DB
Best Local Similarity 100.0%; Pred. No. 0.2;

Best Local Similarity 100.0%; Pled. NO. 0.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGGACCTCCATGT 27

QY I AAAC T CAGTGTGGACCTCCATGTT 27
|||
Db 118 AAAC TTCAGTGTGTGGACCTCCATGTT 144

Search completed: November 19, 2002, 05:17:33
Job time : 1545.46 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	27	100.0	27	10	US-09-829-004A-9		Sequence 9, Appli
2	27	100.0	1350	10	US-09-759-143-616		Sequence 616, App
3	27	100.0	1350	10	US-09-780-669-616		Sequence 616, App
4	27	100.0	1350	10	US-09-822-827-616		Sequence 616, App
5	27	100.0	1729	10	US-09-969-708-598		Sequence 598, App
6	27	100.0	1758	10	US-09-822-827-977		Sequence 977, App
7	27	100.0	2405	10	US-09-822-827-980		Sequence 980, App
8	27	100.0	3423	10	US-09-755-100-5		Sequence 5, Appli
9	27	100.0	3846	10	US-09-755-100-3		Sequence 3, Appli
10	27	100.0	4661	10	US-09-755-100-1		Sequence 1, Appli
11	27	100.0	4661	10	US-09-755-100-2		Sequence 2, Appli
c 12	19.6	72.6	461	10	US-09-969-708-280		Sequence 280, App
c 13	19.6	72.6	601	10	US-09-919-580-72		Sequence 72, Appli
c 14	19.6	72.6	684	10	US-09-919-580-34		Sequence 34, App
15	19.6	72.6	1168	10	US-09-925-300-603		Sequence 603, App
16	18.8	69.6	792	10	US-09-770-445-844		Sequence 844, App
c 17	18.8	69.6	2181	9	US-09-938-842A-1866		Sequence 1866, Ap
18	18.2	67.4	1678	10	US-09-925-300-153		Sequence 153, App
19	18.2	67.4	2417	10	US-09-759-143-334		Sequence 334, App

RESULT 2
US-09-759-143-616
; Sequence 616, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, William
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 616
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-616

Query Match 100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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DB 1129 AAACCTCAGTGTGGACCTCCATGTT 1155

RESULT 3
US-09-780-669-616
Sequence 616, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 616
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-616

Query Match 100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
DB 1129 AAACCTCAGTGTGGACCTCCATGTT 1155

RESULT 4
US-09-822-827-616
Sequence 616, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 616
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapien
US-09-822-827-616

Query Match 100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
DB 1129 AAACCTCAGTGTGGACCTCCATGTT 1155

RESULT 5
US-09-969-708-598
Sequence 598, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 598
LENGTH: 1729
TYPE: DNA
ORGANISM: Homosapiens
US-09-969-708-598

Query Match 100.0%; Score 27; DB 10; Length 1729;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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DB 813 AAACCTCAGTGTGGACCTCCATGTT 839

RESULT 6

US-09-822-827-977
; Sequence 977, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 977
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-977

Query Match 100.0%; Score 27; DB 10; Length 1758;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
Db 1537 AAACCTCAGTGTGGACCTCCATGTT 1563

RESULT 7

US-09-822-827-980
; Sequence 980, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 980
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-980

Query Match 100.0%; Score 27; DB 10; Length 2406;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
Db 1129 AAACCTCAGTGTGGACCTCCATGTT 1155

RESULT 8

US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match 100.0%; Score 27; DB 10; Length 3423;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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Db 2009 AAACCTCAGTGTGGACCTCCATGTT 2035

RESULT 9

US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

Query Match 100.0%; Score 27; DB 10; Length 3846;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
Db 2432 AAACCTCAGTGTGGACCTCCATGTT 2458

RESULT 10

US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match 100.0%; Score 27; DB 10; Length 4661;

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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27
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Db 3247 AACTTCAGTGTGTGGACCTCCATGTT 3273

RESULT 11
US-09-755-100-2
; Sequence 2, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-2

Query Match 100.0%; Score 27; DB 10; Length 4661;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27
    ||||| ||||| ||||| ||||| |||||
Db 3247 AACTTCAGTGTGTGGACCTCCATGTT 3273

RESULT 12
US-09-969-708-280/c
; Sequence 280, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-280

Query Match 72.6%; Score 19.6; DB 10; Length 461;
Best Local Similarity 84.6%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGGACCTCCATGTT 27
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Db 178 AACTTCATTTGTTGGACCTGCATATT 153
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RESULT 13
US-09-919-580-72/c
; Sequence 72, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-72

Query Match 72.6%; Score 19.6; DB 10; Length 601;
Best Local Similarity 84.6%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGGACCTCCATGTT 27
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Db 187 AACTTCATTTGTTGGACCTGCATATT 162

RESULT 14
US-09-919-580-34/c
; Sequence 34, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 89, 92, 122, 123, 295, 320, 322, 352, 355, 361, 369, 375,
; LOCATION: 382, 384, 386, 389, 409, 411, 413, 414, 415, 421, 440, 445,
; LOCATION: 448, 453, 461, 500, 510, 538, 532, 537, 546, 547, 563, 564,
; LOCATION: 569, 577, 583, 587, 597, 598, 599, 609, 613, 616, 621
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 622, 627, 648, 681
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-34

Query Match 72.6%; Score 19.6; DB 10; Length 684;
Best Local Similarity 84.6%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGGACCTCCATGTT 27
    ||||| ||||| ||||| ||||| |||||
Db 198 AACTTCATTTGTTGGACCTGCATATT 173

RESULT 15
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US-09-925-300-603
; Sequence 603, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 603
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1133)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1153)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-603

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Query Match      72.6%; Score 19.6; DB 10; Length 1168;
Best Local Similarity 84.6%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      2  AACTTCAGTGTGGACCTCCATGTT 27
Db      931  AACTTCATGTTTGGACCTGCATATT 956

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GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 00:33:44 ; Search time 912.308 Seconds
(without alignments)
765.605 Million cell updates/sec

Title: US-09-829-004a-7

Perfect score: 24
Sequence: 1 atgtgggtcccggtgtgtcttcctc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
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- 25: em_pl.*
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- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	24	100.0	24	6	AX281250	Sequence
2	24	100.0	70	6	AR147236	Sequence
3	24	100.0	389	9	HSPSA1	Human PSA 9
4	24	100.0	569	9	S75755	PSA-Prostat
5	24	100.0	708	9	HS310937	Human sapi
6	24	100.0	870	9	HS459783	Human sapi
7	24	100.0	876	9	HS459782	Human sapi
8	24	100.0	990	9	HSU17040	Human prost
9	24	100.0	992	6	I67863	Sequence 13
10	24	100.0	1095	9	HS459784	Human sapi
11	24	100.0	1130	9	AF335477	Sequence
12	24	100.0	1446	9	HUMAPS	Human sapien
13	24	100.0	1462	6	I67864	Sequence 14
14	24	100.0	1466	6	E32812	Primer DNA
15	24	100.0	1466	9	HSPSAR	Human mRNA
16	24	100.0	1492	9	EC005307	Human sapi
17	24	100.0	1603	9	HS310938	Human sapi
18	24	100.0	1709	6	AX033403	Sequence
19	24	100.0	1945	9	AF335478	Human sapi
20	24	100.0	2106	6	AX106218	Sequence
21	24	100.0	3423	6	AX033404	Sequence
22	24	100.0	3846	6	AX033402	Sequence
23	24	100.0	4661	6	AX033400	Sequence
24	24	100.0	4661	6	AX033401	Sequence
25	24	100.0	5873	9	HSPSAG	Human DNA f
26	24	100.0	6153	9	HUMPSANTIG	Human prost
27	24	100.0	7130	6	A37262	Sequence 2
28	24	100.0	7130	6	AR167395	Sequence
29	24	100.0	7130	9	HUMPSAA	Human prost
30	24	100.0	40458	9	AC011523	Human sapi
31	24	100.0	217346	2	AC027602	Human sapi
32	24	100.0	230000	9	AF243527	Human sapi
33	20.8	86.7	1514	9	MMPROS	M. mullatta m
34	20	83.3	22	6	AX200977	Sequence
35	20	83.3	22	6	AX267633	Sequence
36	19.8	82.5	2738	5	GGU43396	Gallus gall
37	19.2	80.0	612	6	AX434375	Sequence
38	18.8	78.3	106174	2	AC016126	Human sapi
39	18.8	78.3	139389	9	HS6802	Human DNA S
40	18.8	78.3	158422	9	AC026616	Human sapi
41	18.8	78.3	160709	9	AC115837	Human sapi
42	18.8	78.3	184516	2	AC009629	Human sapi
43	18.4	76.7	1939	9	AK093086	Human sapi
44	18.4	76.7	215241	8	AF459639	Triticum
45	18.2	75.8	3806	8	EN1269479	Emericell

ALIGNMENTS

RESULT 1	AX281250	AX281250	Sequence 7 from Patent WO0176622.	24 bp	DNA	linear	PAT 02-NOV-2001
LOCUS	AX281250	Sequence 7 from Patent WO0176622.					
DEFINITION	AX281250	Sequence 7 from Patent WO0176622.					
ACCESSION	AX281250	Sequence 7 from Patent WO0176622.					
VERSION	AX281250.1	GI:16608506					
KEYWORDS		synthetic construct.					
SOURCE		synthetic construct					
ORGANISM		artificial sequences.					
REFERENCE	1						
AUTHORS	Pedyczak, A., Chong, P. and Sia, C. D.						
TITLE	Immunogenic peptides derived from prostate-specific antigen (psa)						
	and uses thereof						
JOURNAL	Patent: WO 0176622-A 7 18-OCT-2001;						

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FEATURES             source
    source
    Adventis Pasteur Limited (CA)
    Location/Qualifiers
    1..24
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="CLP313"
BASE COUNT          1 a 7 c 7 g 9 t
ORIGIN
Query Match          100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 1 ATGTGGTCCCGGTTGCTTCCTC 24

RESULT 2
AR147236
LOCUS               70 bp DNA linear PAT 08-AUG-2001
DEFINITION          Sequence 2 from patent US 6221579.
ACCESSION            AR147236
VERSION              AR147236.1 GI:15111039
KEYWORDS              Unknown.
SOURCE               Unclassified.
ORGANISM             Everhart,D.S., Kaylor,R.M. and McGrath,K.
REFERENCE            1 (bases 1 to 70)
AUTHORS              Patented binding of functionalized microspheres for optical
TITLE                diffraction-based biosensors
JOURNAL              Patent: US 6221579-A 2 24-APR-2001;
FEATURES             source
    source
    1..70
    /organism="unknown"
BASE COUNT          9 a 19 c 23 g 19 t
ORIGIN
Query Match          100.0%; Score 24; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 25 ATGTGGTCCCGGTTGCTTCCTC 48

RESULT 3
HSPSAL
LOCUS               389 bp DNA linear PRI 24-FEB-1999
DEFINITION          Human PSA gene for prostate specific antigen exon 1.
ACCESSION            X13940
VERSION              X13940.1 GI:35722
KEYWORDS              kallikrein; prostate specific antigen; PSA gene.
SOURCE               Homo sapiens.
ORGANISM             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS              Digby,M.R.
TITLE                Direct Submission
JOURNAL              Submitted (09-JAN-1989) Digby M.R., The Howard Florey Institute,
REFERENCE            Melbourne University, Parkville, Victoria 3052, Australia
AUTHORS              2 (bases 1 to 389)
TITLE                Digby,M., Zhang,X.Y. and Richards,R.I.
JOURNAL              Human prostate specific antigen (PSA) gene: structure and linkage
REFERENCE            to the kallikrein-like gene, hGK-1
AUTHORS              Nucleic Acids Res. 17 (5), 2137 (1989)
MEDLINE              89183632
PUBMED              2467258
COMMENT              Data kindly reviewed (16-may-1989) by Digby M.R.
FEATURES             Location/Qualifiers
    source
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /partial
    /gene="PSA"
    /note="prostate-specific antigen"
    /partial
    /gene="PSA"
    /note="prostate-specific antigen"
    /codon_start=3
    /protein_id="AADI14185.1"
    /db_xref="GI:4261885"
    /translation="POAYHLMPESCVTMMVVPVFLTSLVWIGAAPLLILSRIVGQWEC
    EKHSPQWQVLYASGRVCGVLYHPQWVLTAAHCIRNKSVILLGPHSLFHPEDTCOV
    FQVSHFPLHMLSLANRFRDSSDMLMLRLSEPAFLTDAVKVNDLFTQPEA
    LGTTCTASGWSIEPEFLTKLCQVDL"

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BASE COUNT 108 a 182 c 160 g 119 t
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 569;

Best Local Similarity 100.0%; Pred. No. 0.67; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 ATGTGGTCCCGGTGTCCTTC 24
|||||
Db 42 ATGTGGTCCCGGTGTCCTTC 65

RESULT 5
HSA310937

LOCUS HSA310937 708 bp mRNA linear PRI 17-JAN-2002
DEFINITION Homo sapiens mRNA for putative preproPSA-RP2 (KLK3 gene),
transcript 1.

ACCESSION AJ310937

VERSION AJ310937.1 GI:14422304

KEYWORDS alternative splicing; HKLK3 gene; kallikrein 3; preproPSA-RP2.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1

TITLE Heuze-Vourc'h, N., Leblond, V., Olayat, S., Gauthier, F., and Courty, Y.

CHARACTERIZATION OF PSA-RP2, A PROTEIN RELATED TO PROSTATE-SPECIFIC

ANTIGEN AND ENCODED BY ALTERNATIVE HKLK3 TRANSCRIPTS

Eur. J. Biochem. 268 (16), 4408-4413 (2001)

JOURNAL 21393944

MEDLINE 11502200

PUBMED

REFERENCE 2 (bases 1 to 708)

AUTHORS Courty, Y.

TITLE Direct Submission

JOURNAL Submitted (11-APR-2001) Courty Y., Faculte de Medecine, EMI-U 0010,

Laboratoire d'Enzymologie, 2 bis bd Tonnelle, 37032 Tours cedex,

FRANCE

COMMENT related accession number AJ310938.

FEATURES

source

1..708

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="NH101007.97"

/cell_line="LNCaP"

1..708

/gene="KLK3"

<1..37

/gene="KLK3"

38..580

/gene="KLK3"

/function="unknown"

/note="alternative splicing, transcript 1"

/codon_start=1

/product="putative preproPSA-RP2"

/protein_id="CAC41631.1"

/db_xref="GI:14422305"

/translation="MWVPVFLTSLVTWIGAAPLILSRVGVGWECEKHSPQWVLVAS

RGRVCGVLVHPQVLTAAHCIRNKSVLLGRHSFLFHPEDTGQVFOVSHSPHPLVD

MSLLKNRFLRPGDSSHDMLMLRLSEPAELTDAVKVMDLPTQEPALGTTTCYASGWGSI

EPEETPGDGAAGSPDAWV"

38..88

/gene="KLK3"

110..577

/gene="KLK3"

/product="PSA-RP2"

578..708

/gene="KLK3"

708

/gene="KLK3"

/evidence="experimental"

134 a 214 c 219 g 141 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 708;

Best Local Similarity 100.0%; Pred. No. 0.67; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 ATGTGGTCCCGGTGTCCTTC 24
|||||
Db 38 ATGTGGTCCCGGTGTCCTTC 61

RESULT 6
HSA459783

LOCUS HSA459783 870 bp mRNA linear PRI 09-MAY-2002
DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice
variant 2.

ACCESSION AJ459783

VERSION AJ459783.1 GI:20520642

KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1

TITLE Heuze-Vourc'h, N. and Courty, Y.

COMPLEX ALTERNATIVE SPLICING OF THE HKLK3 GENE CODING FOR THE

TUMOUR MARKER PSA (PROSTATE-SPECIFIC-ANTIGEN)

Unpublished

REFERENCE 2 (bases 1 to 870)

AUTHORS Courty, Y.

TITLE Direct Submission

JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire

d'Enzymologie, Universite F. Rabelais, 2 bis bd Tonnelle, Tours,

37032 cedex, FRANCE

COMMENT alternative splice variant sequences: AJ459782, AJ459784.

FEATURES

Location/Qualifiers

1..870

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="YCI140405-00"

/tissue_type="prostate"

1..870

/gene="KLK3"

22..807

/gene="KLK3"

/note="alternative splice variant 2"

/codon_start=1

/evidence="experimental"

/product="prostate specific antigen"

/protein_id="CAD30845.1"

/db_xref="GI:20520643"

/translation="MWVPVFLTSLVTWIGAAPLILSRVGVGWECEKHSPQWVLVAS

RGRVCGVLVHPQVLTAAHCIRNKSVLLGRHSFLFHPEDTGQVFOVSHSPHPLVD

MSLLKNRFLRPGDSSHDMLMLRLSEPAELTDAVKVMDLPTQEPALGTTTCYASGWGSI

EPEETLPKLCQVDLHVISNDVCAQHPQKTKFNLCAKRWGTXGKSTCGSDSGGPLV

CNGVLQGITSWGSEPCALPERPSLTAKVHYRWKIDTIIVANP"

22..72

/gene="KLK3"

94..804

/gene="KLK3"

/product="prostate specific antigen"

185 a 257 c 242 g 186 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 0.66; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 ATGTGGTCCCGGTGTCCTTC 24
|||||
Db 22 ATGTGGTCCCGGTGTCCTTC 45

RESULT 7
HSA459782

LOCUS HSA459782 876 bp mRNA linear PRI 09-MAY-2002
 DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 1.
 ACCESSION AJ459782
 VERSION AJ459782.1 GI:20520640
 KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Heuze-Vourc'h, N. and Courty, Y.
 TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen).
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 876)
 AUTHORS Courty, Y.
 JOURNAL Direct Submission
 Submitted (03-MAY-2002) Courty, Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabetais, 2 bis bvd Tonnelier, Tours, 37032 cedex, FRANCE
 COMMENT alternative splice variant sequences: AJ459783, AJ459784.
 FEATURES
 source Location/Qualifiers
 1..876
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="YC171105-00"
 /tissue_type="prostate"
 1..876
 /gene="KLK3"
 22..684
 /gene="KLK3"
 /note="alternative splice variant 1"
 /evidence=experimental
 /product="prostate specific antigen"
 /protein_id="CAD30844.1"
 /db_xref="GI:20520641"
 /translation="MWVVFVLTLSVTWIGAAPLILSRIVGWECEKHSQVQVLVAS RGRVCGVLVHPQVLTAAHCRINKSVLLGRHSFLPHEDTGVQVSHSPHGLYV MSLLANRFLRPGDSSDLMLRLSEPAELTDAVKVADLPTQPALGTTCASGSGSI CPREFLTFRKLCQVDLHVISNDVCAQVHPQVTKFMLCAGR WTGGKSTCGSGGFLVCGNVLOGITSWSGSEPCALPERPSLYTKVHYRWIKDTIVA NP".
 sig_peptide 22..72
 mat_peptide 94..681
 /gene="KLK3"
 /product="prostate specific antigen"
 BASE COUNT 220 a 235 c 231 g 190 t
 ORIGIN
 Query Match 100.0%; Score 24; DB 9; Length 876;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
 Db 22 ATGTGGTCCCGGTGTCTTCCTC 45
 RESULT 8
 HSI17040
 LOCUS HSI17040 990 bp mRNA linear PRI 07-DEC-1994
 DEFINITION Human prostate specific antigen precursor mRNA, complete cds.
 ACCESSION U17040
 VERSION U17040.1 GI:595945
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Monne, M.N., Moreno, J.M., Mele, C.M., Mulholland, G.M. and

Gomella, L.G.
 TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence in Benign and Malignant Prostate Tissue
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 990)
 AUTHORS Moreno, J.M.
 JOURNAL Direct Submission
 Submitted (08-NOV-1994) Jose M J.G. Moreno, Urology, Thomas Jefferson University Hospital, 1025 Walnut Street, Philadelphia, PA 19107, USA
 FEATURES
 source Location/Qualifiers
 1..990
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /map="19q13"
 /sex="male"
 /tissue_type="prostate"
 42..827
 /codon_start=1
 /product="prostate specific antigen precursor"
 /protein_id="AAA56764.1"
 /db_xref="GI:595946"
 /translation="MWVVFVLTLSVTWIGAAPLILSRIVGWECEKHSQVQVLVAS RGRVCGVLVHPQVLTAAHCRINKSVLLGRHSFLPHEDTGVQVSHSPHGLYV MSLLANRFLRPGDSSDLMLRLSEPAELTDAVKVADLPTQPALGTTCASGSGSI CPREFLTFRKLCQVDLHVISNDVCAQVHPQVTKFMLCAGR WTGGKSTCGSGGFLV CGNVLOGITSWSGSEPCALPERPSLYTKVHYRWIKDTIVA NP".
 sig_peptide 114..824
 mat_peptide 93..113
 /product="prostate specific antigen"
 /note="propeptide"
 BASE COUNT 209 a 291 c 273 g 217 t
 ORIGIN
 Query Match 100.0%; Score 24; DB 9; Length 990;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
 Db 42 ATGTGGTCCCGGTGTCTTCCTC 65
 RESULT 9
 I67863
 LOCUS I67863 992 bp DNA linear PAT 04-FEB-1998
 DEFINITION Sequence 13 from patent US 5674682.
 ACCESSION I67863
 VERSION I67863.1 GI:2829985
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 992)
 AUTHORS Crooks, C., Gomella, L., Mulholland, S., Grant, J.G. and Nucleic acid primers for detecting micrometastasis of prostate cancer.
 TITLE Patent: US 5674682-A 13 07-OCT-1997;
 JOURNAL Location/Qualifiers
 FEATURES source 1..992
 /organism="unknown"
 BASE COUNT 210 a 291 c 272 g 217 t
 ORIGIN
 Query Match 100.0%; Score 24; DB 6; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
 |||||||

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Db 44 ATGTGGTCCCGGTGTCTTCCTC 67

RESULT 10
HSA459784 1095 bp mRNA linear PRI 09-MAY-2002
LOCUS Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice
DEFINITION variant 3.
ACCESSION AJ459784
VERSION AJ459784.1 GI:20520644
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Heuze-Vourc'h,N. and Courty,Y.
TITLE Complex alternative splicing of the hKLK3 gene coding for the
JOURNAL tumour marker PSA (prostate-specific-antigen)
REFERENCE 2 (bases 1 to 1095)
AUTHORS Courty,Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U-0010, Laboratoire
d'Enzymologie, Universite F. Rabalais, 2 bis bvd Tonnelles, Tours,
37032 cedex, FRANCE
COMMENT alternative splice variant sequences: AJ459782, AJ459783.
FEATURES
source
1..1095
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NH11803.98"
/tissue_type="prostate"
1..1095
/gene="KLK3"
36..352
/gene="KLK3"
/note="alternative splice variant 3"
/codon_start=1
/product="prostate specific antigen"
/protein_id="CAD30846.1"
/db_xref="GI:20520645"
/translation="MMVPPVFLTSLVTWIGRHHGWDAGEGASPDCAEALSPPTQH
PSPDRELGSFLSLPAPLQAHTPSILQSSLPHQVPAPSHLPQNELPPIAQAAPCSQL
Ly"
BASE COUNT 250 a 391 c 196 g 258 t
ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1095;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
|||||
Db 38 ATGTGGTCCCGGTGTCTTCCTC 61

RESULT 11
AF335477 1130 bp mRNA linear PRI 13-MAY-2002
LOCUS Homo sapiens prostate-specific antigen variant 1 mRNA, complete
DEFINITION cds, alternatively spliced.
ACCESSION AF335477
VERSION AF335477.1 GI:18478569
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1130)
AUTHORS David,A., Mabyjeesh,N., Azar,I., Biton,S., Engel,S., Bernstein,J.,
Romano,J., Avdiro,J., Waks,T., Eshhar,Z., Langer,S.Z.,
Lifschitz-Mercer,B., Matzkin,H., Rotman,G., Toporik,A., Savitsky,K.
and Mintz,L.
Unusual alternative splicing within the human kallikrein genes KLK2
and KLK3 gives rise to novel prostate-specific proteins
J. Biol. Chem. 277 (20), 18084-18090 (2002)
22001285
PUBMED 11834722
REFERENCE 2 (bases 1 to 1130)
AUTHORS David,A., Engel,S., Azar,I., Bernstein,J., Rotman,G., Savitsky,K.
and Mintz,L.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Compugen Ltd., 72 Pinchas Rosen, Tel Aviv
69512, Israel
FEATURES
source
1..1130
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.3"
42..356
/note="PSA; KLK3; alternatively spliced"
/codon_start=1
/product="prostate-specific antigen variant 1"
/protein_id="AAL73204.1"
/db_xref="GI:18478570"
/translation="MMVPPVFLTSLVTWIGRHHGWDAGEGASPDCAEALSPPTQH
PSPDRELGSFLSLPAPLQAHTPSILQSSLPHQVPAPSHLPQNELPPIAQAAPCSQL
Ly"
BASE COUNT 213 a 374 c 291 g 252 t
ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
|||||
Db 42 ATGTGGTCCCGGTGTCTTCCTC 65

RESULT 12
HUMAPS 1446 bp mRNA linear PRI 04-JAN-1995
LOCUS Homo sapiens prostate-specific antigen mRNA, complete cds.
DEFINITION M26663
ACCESSION M26663
VERSION M26663.1 GI:618463
KEYWORDS prostate-specific antigen.
SOURCE Homo sapiens prostate gland cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Henttu,P. and Viikko,P.
TITLE CDNA coding for the entire human prostate specific antigen shows
JOURNAL high homologies to the human tissue kallikrein genes
MEDLINE Biochem. Biophys. Res. Commun. 160 (2), 903-910 (1989)
89246551
PUBMED 2470373
COMMENT On Jan 5, 1995 this sequence version replaced gi:341511.
Ref [1] reports bases 1..135 only.
FEATURES
source
1..1446
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19q13.3"
/clone="PSA-20"
/tissue_type="prostate gland"
1..1446
/gene="APS"
1..24
/gene="APS"
/note="G00-119-695"
25..810
/gene="APS"

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/note="AA 18. 24 propeptide; AA 69 glycosylated Asn
residue"
/codon_start=1
/product="prostate-specific antigen"
/protein_id="AAA58802.1"
/db_xref="GI:618464"
/db_xref="GDB:G00-119-695"
/translation="MMVPVFLTSLVWGAAPILSLRIVGCEKHSOPQVVLVAS
MSLKNRFLRPGDSDSHDMLRLSEPAELDAVKVNDLFTQEPALGTCTCYASGWSI
EPEFTPKKLOQVDLHVISNDVCAQHPQKVKFMLCAGRWIGGKSTCGSDGGPLV
25. 75
sig_peptide
/ gene="APS"
/note="G00-119-695"
94. 807
/ gene="APS"
/product="prostate-specific antigen"
811. 1446
/ gene="APS"
/note="G00-119-695"
1446
/ gene="APS"
/note="G00-119-695"
333 a 372 c 419 g 322 t
BASE COUNT
ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1446;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTCCCGTCTCTCTC 24
Db 25 ATGTGGTCCCGTCTCTCTC 48
RESULT 13
LOCUS I67864
DEFINITION Sequence 14 from patent US 5674682.
ACCESSION I67864
VERSION I67864.1 GI:2829986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1462)
AUTHORS Croce,C., Gomella,L., Mulholland,S.,Grant., Moreno,J.G. and
Fischer,R.
TITLE Nucleic acid primers for detecting micrometastasis of prostate
Cancer
JOURNAL Patent: US 5674682-A 14 07-OCT-1997;
FEATURES
Location/Qualifiers
1..1462
/organism="unknown"
BASE COUNT 343 a 374 c 422 g 323 t
ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 1462;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTCCCGTCTCTCTC 24
Db 25 ATGTGGTCCCGTCTCTCTC 48
RESULT 14
LOCUS E32812
DEFINITION Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same.

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ACCESSION E32812
VERSION E32812.1 GI:18623942
KEYWORDS JP 2000069969-A/5.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE unclassified.
1 (bases 1 to 1466)
AUTHORS Nakagawa,H.
TITLE Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same
JOURNAL Patent: JP 2000069969-A 5 07-MAR-2000;
COMMENT HITACHI CHEMICAL CO LTD,KK NIHON IDENSHI KENKYUJO
OS Unidentified
PN JP 2000069969-A/5
PD 07-MAR-2000
PP 28-AUG-1998 JP 1998243419
PR
PI HIROKAZU NAKAGAWARA
PC C12N15/09,C12O1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key: Location/Qualifiers
FT source 1..1466
/organism="Unidentified"
FEATURES
source
Location/Qualifiers
1..1466
/organism="unidentified"
BASE COUNT 338 a 382 c 422 g 324 t
ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 1466;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTCCCGTCTCTCTC 24
Db 44 ATGTGGTCCCGTCTCTCTC 67
RESULT 15
LOCUS HSPSAR
DEFINITION Human mRNA for prostate specific antigen.
ACCESSION X05332
VERSION X05332.1 GI:35740
KEYWORDS antigen; kallikrein-like protein; prostate specific antigen; signal
peptide.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Lundwall,A. and Lilja,H.
TITLE Molecular cloning of human prostate specific antigen cDNA
JOURNAL FEBS Lett. 214 (2), 317-322 (1987)
MEDLINE 87190978
PUBMED 2436946
REFERENCE 2 (bases 1 to 1466)
AUTHORS Lundwall,A.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1989)
COMMENT Data kindly reviewed (01-DEC-1987) by Lundwall A.
FEATURES
Location/Qualifiers
1..1466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lambda HPSA-1"
/tissue_type="prostate"
/clone_lib="(lambda)gt11"
1..1466
notes="primary transcript"
44..829
precursor_RNA
CDS

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/note="precursor polypeptide (AA:17 to 244)"
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Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTTCCTC 24
Db 44 ATGTGGGTCCCGGTGTCTTCCTC 67

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Job time : 920.641 secs

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PA (AVET) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sla CDY;
XX WPI: 2001-663015/76.
DR P-PSDB; AAEL3023.
XX
PM New polypeptide, useful for treating cancers such as prostate cancer,
PM comprises prostate-specific antigen derived peptide
XX
XX Claim 7; Page 28; 41pp; English.
XX
CC The patent discloses immunogenic peptides of prostate-specific antigen
CC (PSA) and nucleic acids encoding them. The peptides of the invention
CC are used to prepare a medicament to elicit an immune response in an
CC animal. They are used to treat cancer such as prostate cancer and
CC tumour metastasis. They are also useful for prophylaxis, for
CC preparing monoclonal or polyclonal antibodies, and in conventional
CC techniques of immunology, molecular biology, cell biology and
CC recombinant DNA technology. The present sequence is a DNA encoding
CC PSA derived peptide, CLP313.
XX
XX Sequence 24 BP; 1 A; 7 C; 7 G; 9 T; 0 other;
SO
Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. NO. 0.15; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTGTCTTCCTC 24
Db 1 ATGTGGTCCCGGTGTCTTCCTC 24
RESULT 2
AAT61707/c
ID AAT61707 standard; cDNA; 27 BP.
XX
AC AAT61707;
XX
DT 24-FEB-1998 (first entry)
XX
DE Prostatic specific antigen antisense oligonucleotide.
XX
KW Human; prostatic specific antigen; probasin; rat; cancer;
XX hyperplasia; antisense oligonucleotide; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..27 a
FT /note= "Phosphorothioated linkages"
XX
XX MO9711172-A1.
XX
PD 27-MAR-1997.
XX
XX 20-SEP-1996; 96MO-US15123.
XX
XX 20-SEP-1995; 95US-0004044.
XX
XX (WORC-) WORCESTER FOUND BIOMEDICAL RES.
XX
XX Zamecnik PA;
XX
XX WPI: 1997-202881/18.
XX
XX Treatment of benign prostatic hyperplasia or prostatic cancer
XX using an anti-sense oligo:nucleotide targeted against prostate
XX specific antigen or the probasin gene
XX
XX Claim 6; Page 38; 49pp; English.
XX
XX A novel method has been developed for treating a patient diagnosed as

CC having benign prostatic hyperplasia or a prostatic cancer. The method
CC comprises administering to the patient a therapeutic amount of a
CC composition comprising an antisense oligonucleotide which selectively
CC hybridises to prostate specific antigen (PSA) gene or mRNA or to a
CC probasin gene or mRNA sequence of the patient, where the antisense
CC oligonucleotide inhibits expression of the sequence. The present
CC sequence represents a specifically claimed antisense oligonucleotide
CC against prostatic specific antigen. The antisense oligonucleotide can
CC be used to effectively inhibit the growth of (and for the killing of)
CC hyperplastic cells or cancerous cells of prostatic origin. Expression
CC of the PSA and probasin genes is specific to prostatic cells so that the
CC antisense oligonucleotide can be administered systemically, making it
CC particularly useful in late stage prostatic cancer which has
CC metastasised, and in which the cells have become resistant to oestrogen
CC or anti-androgen therapy. The method can also be used in benign prostatic
CC hyperplasia, or early stage prostatic cancer, as an alternative for the
CC more radical procedures currently used, such as transurethral resection,
CC radical prostatectomy, or physical or chemical castration.
XX
XX Sequence 27 BP; 9 A; 7 C; 9 G; 2 T; 0 other;
SO
Query Match 100.0%; Score 24; DB 18; Length 27;
Best Local Similarity 100.0%; Pred. NO. 0.16; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTGTCTTCCTC 24
Db 27 ATGTGGTCCCGGTGTCTTCCTC 4
RESULT 3
AAT35293
ID AAT35293 standard; DNA; 45 BP.
XX
AC AAT35293;
XX
DT 11-MAR-1997 (first entry)
XX
DE Forward primer F1 for prostate specific antigen.
XX
XX Polymerase chain reaction; primer; amplify; prostate specific antigen;
XX baculovirus transfer vector; PCR; PSA; ss.
XX
XX Synthetic.
XX
XX BP725139-A2.
XX
PD 07-AUG-1996.
XX
XX 31-JAN-1996; 96EP-0101304.
XX
XX 28-APR-1995; 95US-0430498.
XX
XX 03-FEB-1995; 95US-0383111.
XX
XX (FARB) BAYER CORP.
XX
XX Barnett TR, Ng PC, Yeung KK;
XX
XX WPI: 1996-356106/36.
XX
XX Recombinant prostate-specific antigen (PSA) and immunological
XX fragments - for use as an immunoassay calibrator in commercial PSA
XX tests.
XX
XX Claim 3; Page 5; 19pp; English.
XX
XX AAT35293-r35295 represent amplification primers for the prostate
XX specific antigen (PSA). These primers were used to insert the cDNA for
XX PSA into a BamHI-NciI-cleaved pVL1393 baculovirus transfer vector. The
XX vector that was produced is ATCC VR-2496. The rPSA can be produced by the
XX use of the rPSA are for the quantitative determination of PSA in a
XX biological sample. In the assay, the test sample is combined with a

CC labelled conjugate and the response of the conjugate is compared to a
CC standard curve established by performing the assay on one or more
CC calibrators using RPSA (or an immunologically reactive fragment).

XX Sequence 45 BP; 4 A; 15 C; 12 G; 14 T; 0 other;

Query Match 100.0%; Score 24; DB 17; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGCTCTCTC 24

DB 16 ATGTGGTCCCGGTGCTCTCTC 39

RESULT 4
ABN36013
ID ABN36013 standard; DNA; 60 BP.

XX ABN36013;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:8761.

XX Human: mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI: 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX

PS Example 1; SEQ ID 8761; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample. In expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN35389 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 60 BP; 6 A; 17 C; 18 G; 19 T; 0 other;

Query Match 100.0%; Score 24; DB 24; Length 60;

Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGCTCTCTC 24

DB 13 ATGTGGTCCCGGTGCTCTCTC 36

RESULT 5
AAA63192
ID AAA63192 standard; DNA; 70 BP.

XX AAA63192;

DT 02-FEB-2001 (first entry)

DE Nucleic acid used as an analyte in a diffraction-based biosensor assay.

XX Optical diffraction-based biosensor; analyte detection;
KW contamination; infection; cancer; ss.

XX Synthetic.

OS Key Location/Qualifiers

FT modified_base 1 /tag= a

FT /mod_base= OTHER

FT /note= "Biotin-5'."

PN WO200034781-A2.

PD 15-JUN-2000.

PF 22-NOV-1999; 99WO-US27671.

PR 11-DEC-1998; 98US-0210016.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Everhart DS, Kaylor RM, McGrath K;

DR WPI: 2000-475352/41.

XX Diffraction-based analyte detection, useful for clinical diagnosis of
PT infections and cancer, comprises reacting analyte with
PT diffraction-enhancing material carrying specific receptor
XX

PS Example 2; Page 23; 38pp; English.

XX The present invention relates to a method for detecting and quantifying
CC the presence or amount of an analyte within a medium. The method
CC comprises micro-contact printing of analyte-specific receptors onto
CC polymer film. The target analyte binds to the polymer film, and results
CC in light diffraction when light is transmitted through the film. The
CC analyte can be detected by analysing the diffraction pattern of the
CC transmitted light. The method of the present invention may be used to detect
CC and quantify a variety of analytes; e.g. microorganisms, viruses, nucleic
CC acids, hormones, steroids, antibodies, drugs, metals and antigens, either
CC for clinical diagnosis of infections, cancer and allergies or for
CC detecting microbial contamination of garments. The present sequence is a
CC synthetic oligonucleotide, which was used as an analyte to illustrate the
CC present invention.

XX Sequence 70 BP; 9 A; 19 C; 23 G; 19 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 70;

Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 25 ATGTGGTCCCGGTTGCTTCCTC 48

RESULT 6
ABL60747
ID ABL60747 standard; DNA; 90 BP.
XX
AC ABL60747;
XX
DT 10-SEP-2002 (first entry)
XX
DE Prostate specific antigen (PSA) fragment encoding DNA.
XX
KM Prostate specific antigen; PSA; prostate; cancer; prostatic disease;
XX gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1..90
FT /tag= a
FT /product= "PSA"
FT /note= "partial fragment"
FT 1..72
FT /tag= b
FT /note= "preproPSA"
FT 52..72
FT /tag= c
FT /note= "PropSA"
FT 73..90
FT mat_peptide
FT /tag= d
FT /note= "partial mature PSA"
XX
PN US2002045198-A1.
XX
PD 18-APR-2002.
XX
PE 23-FEB-2001; 2001US-0792534.
XX
PR 30-APR-1999; 99US-0302965.
XX
PA (MIKO/) MIKOLAJCZYK S D.
PA (RITT/) RITTENHOUSE H G.
PA (WANG/) WANG T J.
PA (WOLF/) WOLFERT R L.
XX
PI Mkolajczyk SD, Rittenhouse HG, Wang TJ, Wolfert RL;
XX WPI: 2002-425439/45.
XX
DR P-PSDB; ABB08071.
XX
PT Determining prostate specific antibody (PSA), comprises determining
PT the amount of complex formed on treating a sample with a PSA specific
PT antibody, useful for detecting prostate cancer and distinguishing it
PT from benign prostatic disease
XX
PS Disclosure; Fig 1: 30pp; English.
XX
CC The invention provides a method of determining prostate specific antigen
CC (PSA) in a sample which involves determining the amount of complex
CC formed on treating a sample with a PSA specific antibody. The method is
CC useful for detecting prostate cancer and distinguishing it from benign
CC prostatic disease. The present sequence represents a DNA encoding a
CC partial fragment of the PSA.
XX
SQ Sequence 90 BP; 8 A; 26 C; 31 G; 25 T; 0 other;
Query Match 100.0%; Score 24; DB 24; Length 90;

Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 1 ATGTGGTCCCGGTTGCTTCCTC 24

RESULT 7
AAT92974
ID AAT92974 standard; cDNA; 92 BP.
XX
AC AAT92974;
XX
DT 24-APR-1998 (first entry)
XX
DE cDNA for prostate specific antigen (PSA).
XX
KM Diagnosis; prostate cancer; prostate specific antigen; PSA;
KM metastatic prostate cancer; prostate cell; secondary tumour;
KM bone metastatic anchoring; ss.
XX
OS Homo sapiens.
XX
FH Homo sapiens.
XX
PN WO9739139-A1.
XX
PD 23-OCT-1997.
XX
PE 16-APR-1997; 97WO-US06497.
XX
PR 16-APR-1996; 96US-0015765.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Robbins DJ;
XX
DR WPI: 1997-526473/48.
XX
PT Monitoring or diagnosis of prostate cancer - by detecting
PT prostate-specific antigen mRNA using specific primers
XX
PS Disclosure; Page 13; 25pp; English.
XX
CC cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
CC The detection of PSA mRNA in peripheral blood is associated with
CC metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
CC indicates that prostate cells are circulating in the blood and confirms
CC diagnosis of cancer. Circulating prostate cells also indicate a risk of a
CC secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
CC after prostatectomy or radiotherapy indicates a risk that the prostate
CC cancer has spread and that the surgery and radiotherapy was not
CC effective. PCR primers AAT92971-73 were used for the monitoring and
CC diagnosis of patients with prostate cancer. The method comprises the
CC detection of PSA mRNA by reverse transcriptase polymerase chain reaction
CC (RT-PCR).
XX
SQ Sequence 92 BP; 14 A; 28 C; 28 G; 22 T; 0 other;
Query Match 100.0%; Score 24; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 38 ATGTGGTCCCGGTTGCTTCCTC 61
RESULT 8
AAT35294
ID AAT35294 standard; DNA; 93 BP.
XX
AC AAT35294;
XX

DT 11-MAR-1997 (first entry)
XX Forward primer F2 for prostate specific antigen.
DE Polymerase chain reaction; primer; amplify; prostate specific antigen;
XX baculovirus transfer vector; PCR; PSA; ss.
KM Synthetic.
XX EP725139-A2.
XX 07-AUG-1996.
XX 31-JAN-1996; 96EP-0101304.
PF 28-APR-1995; 950S-0430498.
PR 03-FEB-1995; 950S-0383111.
XX (FARB) BAYER CORP.
XX Barnett TR, Ng PC, Yeung KK;
PI WPI; 1996-356106/36.
DR Recombinant prostate-specific antigen (PSA) and immunological
XX fragments - for use as an immunoassay calibrator in commercial PSA
PT tests.
PT Claim 3; Page 5; 19pp; English.
PS AAT35293-T35295 represent amplification primers for the prostate
XX specific antigen (PSA). These primers were used to insert the cDNA for
CC PSA into a BamHI-NOTI-cleaved pVL393 baculovirus transfer vector. The
CC vector that was produced is ATCC VR-2496. The PSA can be produced by the
CC use of the rPSA are for the quantitative determination of PSA in a
CC biological sample. In the assay, the test sample is combined with a
CC labelled conjugate and the response of the conjugate is compared with a
CC standard curve established by performing the assay on one or more
CC calibrators using rPSA (or an immunologically reactive fragment).
XX
SQ Sequence 93 BP; 12 A; 23 C; 31 G; 27 T; 0 other;
Query Match 100.0%; Score 24; DB 17; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 0; Gaps 0;
QY 1 ATGTGGGTCCCGGTGTCTCTCCTC 24
Db 16 ATGTGGGTCCCGGTGTCTCTCCTC 39
RESULT 9
ABV07911
ID ABV07911 standard; cDNA; 171 BP.
XX
AC ABV07911;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 7902.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX

PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
DR Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 1267; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
SQ Sequence 171 BP; 20 A; 55 C; 51 G; 43 T; 2 other;
Query Match 100.0%; Score 24; DB 23; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 0; Gaps 0;
QY 1 ATGTGGGTCCCGGTGTCTCTCCTC 24
Db 79 ATGTGGGTCCCGGTGTCTCTCCTC 102
RESULT 10
ABV07396
ID ABV07396 standard; cDNA; 308 BP.
XX
AC ABV07396;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 7387.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX

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XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 1194; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 308 BP; 65 A; 100 C; 79 G; 63 T; 1 other;
SQ
Query Match 100.0%; Score 24; DB 23; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTTGTTCTTC 24
DB 198 ATGTGGTCCCGGTTGTTCTTC 221

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XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 7668; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 428 BP; 82 A; 132 C; 123 G; 91 T; 0 other;
SQ
Query Match 100.0%; Score 24; DB 23; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTTGTTCTTC 24
DB 271 ATGTGGTCCCGGTTGTTCTTC 294

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Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rng

Page 8

Db 62 ATGTGGTCCGGTGTCTCTCCTC 85

RESULT 15

AAZ47134
ID AAZ47134 standard; DNA; 990 BP.

AC AAZ47134;

DT 28-MAR-2000 (first entry)

DE Human prostate-specific antigen gene.

KW Immunization; prostate cancer; prostate-specific antigen; PSA;

OS Homo sapiens.

PN WO9961068-A1.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US12072.

PR 29-MAY-1998; 98US-0087305.

PA (TYPE-) UNIV PENNSYLVANIA.

PI Weiner DB, Kim JJ;

DR WPI; 2000-072551/06.

XX P-PSDB; AAY56048.

PT Immunization against prostatic cancer using nucleic acid encoding

XX prostate-specific antigen, for treatment or prophylaxis

PS Disclosure; Page 42; 47pp; English.

CC The invention relates to a method of immunization against prostatic

CC cancer (PC) by administering a nucleic acid (this sequence) that encodes

CC prostate-specific antigen (PSA), or its immunologically active fragment

CC operably linked to regulatory sequences. The nucleic acid is taken up by

CC cells and then expressed to generate an immune response against PSA.

CC The method is used to protect against, or treat, PC, or more generally

CC to induce a cellular immune response to PSA.

XX

SO Sequence 990 BP; 209 A; 291 C; 273 G; 217 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 990;

Best Local Similarity 100.0%; Pred.No. 0.21; 0; Mismatches 0;

Matches 24; Conservative 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCGGTGTCTCTCCTC 24

Db 42 ATGTGGTCCGGTGTCTCTCCTC 65

Search completed: November 19, 2002, 03:06:36

Job time: 171.462 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 ; Search time 1371.08 Seconds
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Title: US-09-829-004A-7

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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5: em_estlov:*
6: em_estlpl:*
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8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
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21: em_gsa_vrt:*
22: em_gsa_fun:*
23: em_gsa_mam:*
24: em_gsa_mus:*
25: em_gsa_other:*
26: em_gsa_pro:*
27: em_gsa_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	316	9	AA593245
2	24	100.0	336	9	AA506459
3	24	100.0	371	9	AA503943
4	24	100.0	391	9	AA506939
5	24	100.0	408	12	BF678836
6	24	100.0	457	9	AA528287

7	24	100.0	465	13	B1046475	
c <td>8</td> <td>24</td> <td>100.0</td> <td>495</td> <td>12</td> <td>BE840533</td>	8	24	100.0	495	12	BE840533
c <td>9</td> <td>24</td> <td>100.0</td> <td>505</td> <td>12</td> <td>BE840441</td>	9	24	100.0	505	12	BE840441
10	24	100.0	523	9	AA639901	
11	24	100.0	532	12	BE840701	
c <td>12</td> <td>24</td> <td>100.0</td> <td>572</td> <td>12</td> <td>BE840537</td>	12	24	100.0	572	12	BE840537
13	24	100.0	591	12	BF679591	
14	24	100.0	638	12	BF679511	
15	24	100.0	648	12	BF67605	
16	24	100.0	672	9	A1524893	
17	24	100.0	724	12	BE964653	
18	24	100.0	732	9	A1547309	
19	24	100.0	737	9	A1547285	
20	24	100.0	748	12	BF679168	
21	24	100.0	748	12	BE973983	
22	24	100.0	756	12	BE676011	
23	24	100.0	763	12	BF965254	
24	24	100.0	770	12	BF675749	
25	24	100.0	784	12	BF678386	
26	24	100.0	788	12	BF675771	
27	24	100.0	794	12	BE675511	
28	24	100.0	796	12	BE674927	
29	24	100.0	797	12	BF675142	
30	24	100.0	813	12	BF681507	
31	24	100.0	825	12	BF677556	
32	24	100.0	828	12	BF678076	
33	24	100.0	832	9	A1557311	
34	24	100.0	838	12	BF680970	
35	24	100.0	841	12	BF673766	
36	24	100.0	843	12	BF675323	
37	24	100.0	849	12	BF673243	
38	24	100.0	859	12	BF675660	
39	24	100.0	860	12	BE675331	
40	24	100.0	866	12	BE965220	
41	24	100.0	868	12	BF673807	
42	24	100.0	871	12	BF673369	
43	24	100.0	873	12	BF678012	
44	24	100.0	888	12	BF681002	
45	24	100.0	890	14	BQ949420	

ALIGNMENTS

RESULT 1
AA593245
LOCUS
DEFINITION
AA593245 316 bp mRNA
n07e10.s1 NCI CGAP P74.1 Homo sapiens CDNA clone IMAGE:1077066
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN),
mRNA sequence.
ACCESSION
AA593245
VERSION
AA593245.1 GI:2409007
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 316)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 427 Std Error: 0.00

Tue Nov 19 15:43:52 2002

us-09-829-004a-7.rst

Page 2

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 293.
Location/Qualifiers

FEATURES

source

1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1077066"
/clone_lib="NCI_CGAP_P4.1"
/sex="male"
/tissue_type="prostatic intraepithelial neoplasia - high grade"
/lab_host="DH10B"
/note="Organ: prostate; Vector: PAMP10; mRNA made from prostatic intraepithelial neoplasia (high-grade), CDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. CDNA library preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. CDNA library arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center"

BASE COUNT 52 a 93 c 98 g 73 t
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGTGGTCCCGTTGCTCTC 24
|||||
25 ATGTGGTCCCGTTGCTCTC 48

RESULT 2 336 bp mRNA linear EST 20-AUG-1997
AA506459
LOCUS nh46a08.s1 NCI CGAP P45 Homo sapiens CDNA clone IMAGE:955382
DEFINITION similar to gb:M1895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
mRNA sequence.

ACCESSION AA506459.1 GI:2242699
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 336)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-ri@mail.nih.gov
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA library preparation: David B. Krizman, Ph.D.
CDNA library arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert length: 442 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

LOCATION/Qualifiers

FEATURES

source

1..336
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/clone_image="IMAGE:955382"
/clone_lib="NCI_CGAP_P45"
/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/note="Vector: PAMP10; mRNA made from normal prostatic

epithelial cells, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp.
BASE COUNT 57 a 106 c 99 g 74 t
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGTGGTCCCGTTGCTCTC 24
|||||
33 ATGTGGTCCCGTTGCTCTC 56

RESULT 3 371 bp mRNA linear EST 20-AUG-1997
AA503943
LOCUS nh38d05.s1 NCI CGAP P45 Homo sapiens CDNA clone IMAGE:954633
DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
mRNA sequence.

ACCESSION AA503943.1 GI:2238910
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 371)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-ri@mail.nih.gov
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA library preparation: David B. Krizman, Ph.D.
CDNA library arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/dbp/image/image.html
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Seq primer: -40ml3 fwd. ET from Amersham.

LOCATION/Qualifiers

FEATURES

source

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/clone_image="IMAGE:954633"
/clone_lib="NCI_CGAP_P45"
/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/note="Vector: PAMP10; mRNA made from normal prostatic
epithelial cells, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp.
BASE COUNT 63 a 112 c 111 g 85 t
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGTGGTCCCGTTGCTCTC 24
|||||
27 ATGTGGTCCCGTTGCTCTC 50

RESULT 4
AA506939/c

LOCUS AA506939 391 bp mRNA linear EST 20-AUG-1997
 DEFINITION nh6407.s1 NCI CGAP Pr8 Homo sapiens CDNA clone IMAGE:957109
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA506939 GI:2243378
 VERSION AA506939.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 391)
 NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 488 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amerisham.
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:957109"
 /clone_lib="NCI_CGAP_Pr8"
 /sex="male"
 /tissue_type="prostate"
 /lab_host="DH10B"
 /note="Vector: PAMP10; mRNA made from invasive prostate
 tumor. CDNA made by oligo-dT priming. Non-directionally
 cloned. Size-selected on agarose gel, average insert
 size 600 bp." 87 a 96 c 138 g 70 t
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 24; DB 9; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Gaps 0;
 Matches 24; Conservative 0; Indels 0; Gaps 0;
 QY 1 ATGTGGTCCCGGTGCTCTCTC 24
 ||||||||||||||||||||
 Db 384 ATGTGGTCCCGGTGCTCTCTC 361
 RESULT 5
 LOCUS BF678836 408 bp mRNA linear EST 21-DEC-2000
 DEFINITION 60215313.f1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4294258 5',
 mRNA sequence.
 ACCESSION BF678836
 VERSION BF678836.1 GI:11952731
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 408)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM1143 row: e column: 11
 High quality sequence stop: 407
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 Location/Qualifiers
 1..408
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 /db_xref="taxon:9606"
 /clone="IMAGE:4294258"
 /clone_lib="NIH_MGC_83"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcgcttcggcc); Site_2: SfiI (ggcctatggc
); 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 clones
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."
 74 a 127 c 115 g 92 t
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 24; DB 12; Length 408;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Gaps 0;
 Matches 24; Conservative 0; Indels 0; Gaps 0;
 QY 1 ATGTGGTCCCGGTGCTCTCTC 24
 ||||||||||||||||||||
 Db 37 ATGTGGTCCCGGTGCTCTCTC 60
 RESULT 6
 LOCUS AA528287 457 bp mRNA linear EST 20-AUG-1997
 DEFINITION nh2608.s1 NCI CGAP Pr3 Homo sapiens CDNA clone IMAGE:953487
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA528287 GI:2270356
 VERSION AA528287
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 457)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: W. Marston Linahan, M.D., Rodrigo Chuagui, M.D.
 Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. ET from Amerisham
 High quality sequence stop: 187
 FEATURES
 source
 Location/Qualifiers
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 /clone="IMAGE:953487"
 /clone_lib="NCI_CGAP_Pr3"
 /sex="male"

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/dev.stage="45 years old"
/lab.host="PH10b"
/Note="vector: PAMP10; Site 1: Not1; Site 2: EcoR1; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoR1 adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDC-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."

BASE COUNT      79 a      160 c      112 g      106 t
ORIGIN

Query Match      100.0%; Score 24; DB 9; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 26 ATGTGGTCCCGGTTGCTTCCTC 49

RESULT 7
BI046475      465 bp      mRNA      linear      EST 14-JUN-2001
LOCUS      MR3-FN0209-070201-010-b11 FN0209 Homo sapiens cDNA, mRNA sequence.
DEFINITION      BI046475
ACCESSION      BI046475
VERSION      BI046475.1 GI:14453097
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 465)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3at2-MR3-FN0209-
070201-010-b11&f3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 465.
Location/Qualifiers
1. 465
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/clone_lib="FN0209"
/dev.stage="Adult"
/Note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTS PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse

JOURNAL
MEDLINE
COMMENT
AUTHORS
REFERENCE
1 (bases 1 to 465)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3at2-MR3-FN0209-
070201-010-b11&f3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 465.
Location/Qualifiers
1. 465
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0209"
/dev.stage="Adult"
/Note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTS PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse

BASE COUNT      100.0%; Score 24; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 463 ATGTGGTCCCGGTTGCTTCCTC 440

transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT      83 a      134 c      144 g      103 t
ORIGIN

Query Match      100.0%; Score 24; DB 13; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCCGGTTGCTTCCTC 24
|||||
Db 167 ATGTGGTCCCGGTTGCTTCCTC 190

RESULT 8
BE840533/c      495 bp      mRNA      linear      EST 22-SEP-2000
LOCUS      RC1-FN0188-260700-022-F06 FN0188 Homo sapiens cDNA, mRNA sequence.
DEFINITION      BE840533
ACCESSION      BE840533
VERSION      BE840533.1 GI:10272911
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 495)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1-FN0188-260
700-022-F06&f3=2000-07-26&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 495.
Location/Qualifiers
1. 495
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0188"
/dev.stage="Adult"
/Note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTS PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

```

RESULT 9
 BE840441/c 505 bp mRNA linear EST 22-SEP-2000
 LOCUS RCL-FN0188-210700-021-a02 FN0188 Homo sapiens CDNA, mRNA sequence.
 DEFINITION BE840441
 ACCESSION BE840441.1 GI:10272819
 VERSION EST.
 KEYWORDS human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 505)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202653
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-RCL-FN0188-210700-021-a02&t3=2000-07-21&t4=1)
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 High quality sequence stop: 505.
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 /clone_lib="FN0188"
 /dev_stage="Adult"
 /note="Organ: prostate, normal; Vector: puc18; Site_1: SmaI ; Site_2: SmaI. A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 127 a 164 c 136 g 78 t
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 Db 460 ATGTGGTCCCGGTGTCTCTC 437
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 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA639901
 VERSION AA639901.1 GI:2563680
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 523)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagut, M.D.,
 Michael Emmert-Buck, M.D., Ph.D.,
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bdip/image/image.html
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 367.
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 /clone_lib="NCI-CGAP_Pt3"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kitzman."
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 Best Local Similarity 100.0%; Pred. No. 1.9;
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 Db 32 ATGTGGTCCCGGTGTCTCTC 55
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 DEFINITION RCL-FN0188-140800-011-g05 FN0188 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BE840701
 VERSION BE840701.1 GI:10273079
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 552)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

BASE COUNT 116 a 181 c 166 g 128 t
ORIGIN

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCGGTGTCTCTCCTC 24
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DEFINITION mRNA sequence.
ACCESSION BF679511
VERSION BF679511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 638)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1145 row: k column: 05
High quality sequence stop: 633.

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/clone_lib="NIH_MGC_83"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgctgccc); Site 2: SfiI (ggccatgatgccc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dt(30)BN-3',
sequence: 5'-ATTCTAGAGCGCGGCGGCGGCGACATG-dt(30)BN-3',
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 86 a 190 c 182 g 180 t
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Query Match 100.0%; Score 24; DB 12; Length 638;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 43 ATGTGGGTCCGGTGTCTCTCCTC 66

RESULT 15
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LOCUS 602085679P1 NIH_MGC_83 Homo sapiens cDNA IMAGE:4249939 5',
DEFINITION

RNA sequence.
BF677605
BF677605.1 GI:11951500
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 648)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1070 row: n column: 20
High quality sequence stop: 611.

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/clone_lib="NIH_MGC_83"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgctgccc); Site 2: SfiI (ggccatgatgccc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGGCGACATG-dt(30)BN-3',
sequence: 5'-ATTCTAGAGCGCGGCGGCGGCGGCGACATG-dt(30)BN-3',
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 124 a 198 c 185 g 141 t
ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 648;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCGGTGTCTCTCCTC 24
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DB 43 ATGTGGGTCCGGTGTCTCTCCTC 66

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Job time : 1377.08 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 47.0769 seconds
(without alignments)
156.345 Million cell updates/sec

Title: US-09-829-004A-7

Perfect score: 24
Sequence: 1 atgtggtccggtgtgtctctc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	70	4	US-09-210-016-2 Sequence 2, Appl
2	24	100.0	111	1	US-08-454-720A-42 Sequence 42, Appl
3	24	100.0	992	1	US-08-358-782D-13 Sequence 13, Appl
4	24	100.0	992	2	US-08-764-527A-13 Sequence 13, Appl
5	24	100.0	1462	1	US-08-358-782D-14 Sequence 14, Appl
6	24	100.0	1462	2	US-08-764-527A-14 Sequence 14, Appl
7	24	100.0	7130	4	US-09-056-105-31 Sequence 31, Appl
8	20	83.3	22	4	US-09-605-785-607- Sequence 607, App
9	18	75.0	28	1	US-08-394-033-1 Sequence 1, Appl
10	18	75.0	2153	2	US-08-577-492-31 Sequence 31, Appl
11	18	75.0	2153	4	US-09-079-630-31 Sequence 31, Appl
12	17.6	73.3	1348	4	US-09-042-071-19 Sequence 19, Appl
13	16.4	68.3	1864	4	US-08-454-720A-38 Sequence 38, Appl
14	16	66.7	72	4	US-08-983-075D-10 Sequence 10, Appl
15	16	66.7	558	4	US-09-385-982-435 Sequence 435, App
16	16	66.7	832	4	US-09-100-264-8 Sequence 8, Appl
17	16	66.7	832	3	US-08-768-859A-5 Sequence 5, Appl
18	16	66.7	832	3	US-08-768-859A-20 Sequence 20, Appl
19	16	66.7	832	3	US-08-767-820A-5 Sequence 5, Appl
20	16	66.7	832	3	US-08-767-820A-20 Sequence 20, Appl
21	16	66.7	832	3	US-08-622-046B-4 Sequence 4, Appl
22	16	66.7	832	3	US-08-622-046B-15 Sequence 15, Appl
23	16	66.7	832	5	PCT-US95-06157-5 Sequence 5, Appl
24	16	66.7	833	2	US-08-790-137-2 Sequence 2, Appl
25	16	66.7	871	1	US-08-744-026-2 Sequence 2, Appl
26	16	66.7	871	2	US-09-102-732-2 Sequence 2, Appl
27	16	66.7	871	4	US-09-261-767-2 Sequence 2, Appl

28	16	66.7	871	4	US-08-969-987-7 Sequence 7, Appl
29	16	66.7	1279	3	US-08-985-950-5 Sequence 5, Appl
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31	16	66.7	1358	4	US-08-983-075D-8 Sequence 8, Appl
32	16	66.7	1728	3	US-08-985-950-7 Sequence 7, Appl
33	15.8	65.8	424	1	US-08-158-189-4 Sequence 4, Appl
34	15.8	65.8	2880	1	US-08-158-189-1 Sequence 1, Appl
35	15.6	65.0	340	4	US-08-836-075A-99 Sequence 99, Appl
36	15.6	65.0	1508	4	US-09-404-390-14 Sequence 14, Appl
37	15.6	65.0	2333	4	US-09-404-390-15 Sequence 15, Appl
38	15.6	65.0	8051	2	US-08-576-626A-2 Sequence 2, Appl
39	15.2	63.3	1512	2	US-07-938-154-10 Sequence 10, Appl
40	15.2	63.3	1512	5	PCT-US91-02311-10 Sequence 10, Appl
41	15.2	63.3	2241	2	US-08-838-219B-20 Sequence 20, Appl
42	15.2	63.3	2241	3	US-09-233-336A-20 Sequence 20, Appl
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44	15.2	63.3	2241	4	US-09-402-036-20 Sequence 20, Appl
45	15.2	63.3	2241	4	US-09-904-226-20 Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-09-210-016-2
; Sequence 2, Application US/09210016
; Patent No. 6221579
; GENERAL INFORMATION:
; APPLICANT: Everhart, Dennis S.
; APPLICANT: Kaylor, Rosann M.
; APPLICANT: McGeath, Kevin
; TITLE OF INVENTION: Patterned Binding of Functionalized Microspheres for
; TITLE OF INVENTION: Optical Diffraction-Based Biosensors
; FILE REFERENCE: 11301-0880
; CURRENT APPLICATION NUMBER: US/09/210,016
; CURRENT FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
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Db 25 ATGTGGTCCCGGTGCTCTCTC 48
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; Sequence 42, Application US/08454720A
; Patent No. 5766888
; GENERAL INFORMATION:
; APPLICANT: Sobol, Robert E.
; APPLICANT: Green, Mark R.
; APPLICANT: Kawasaki, Ernest S.
; TITLE OF INVENTION: Detection of Carcinoma Metastases by
; TITLE OF INVENTION: Nucleic Acid Amplification
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffman-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
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Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rni

Page 2

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ZIP: 07110
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.01, version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,720A
FILING DATE: May 31, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/357,565
FILING DATE: December 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 9178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2974
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-720A-42

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Best Local Similarity 100.0%; Prcd. No. 0.023;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ATGTGGGTCCCGGTGTCTTCTC 24
Db 1 ATGTGGGTCCCGGTGTCTTCTC 24

RESULT 3
US-08-358-782D-13
Sequence 13, Application US/08358782D
Patent No. 5674682
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gomella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:

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SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-13

Query Match
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCGGTGTCTCTCTC 24
Db 44 ATGTGGTCCGGTGTCTCTCTC 67

RESULT 4
US-08-764-527A-13
Sequence 13, Application US/08764527A
Patent No. 5939258
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Comella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
TITLE OF INVENTION: Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TUD-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-13

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCGGTGTCTCTCTC 24
Db 44 ATGTGGTCCGGTGTCTCTCTC 67

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Db 44 ATGTGGGTCCCGGTGTCTTCCTC 67

RESULT 5

US-08-358-782D-14

Sequence 14, Application US/08358782D

Patent No. 5674682

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

APPLICANT: Gomeila, Leonard

APPLICANT: Mulholland, S. Grant

APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer

TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

CITY: Philadelphia

STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,782D

FILING DATE: 15-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: TJU-1327

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1462 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-358-782D-14

Query Match

Best Local Similarity 100.0%; Score 24; DB 1; Length 1462;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

US-08-764-527A-14

Sequence 14, Application US/08764527A

Patent No. 5939258

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

APPLICANT: Gomeila, Leonard

APPLICANT: Mulholland, S. Grant

APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer

TITLE OF INVENTION: Methods of Detecting Micrometastasis of

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

STREET: One Liberty Place 46th. Floor

CITY: Philadelphia

STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,527A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/358,782

FILING DATE: 15-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: TJU-1327

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1462 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-764-527A-14

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 1462;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 ATGTGGGTCCCGGTGTCTTCCTC 48

RESULT 7

US-09-056-105-31

Sequence 31, Application US/09056105

Patent No. 6287569

GENERAL INFORMATION:

APPLICANT: KIPPS, THOMAS J.

APPLICANT: MU, YUNQI

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

FILE REFERENCE: 233/221

CURRENT APPLICATION NUMBER: US/09/056,105

CURRENT FILING DATE: 1998-04-06

EARLIER APPLICATION NUMBER: 60/043,467

EARLIER FILING DATE: 1997-04-10

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 7130

TYPE: DNA

ORGANISM: Homo sapiens

US-09-056-105-31

Query Match

Best Local Similarity 100.0%; Score 24; DB 4; Length 7130;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 675 ATGTGGGTCCCGGTGTCTTCCTC 698

RESULT 8

US-09-056-105-31

Sequence 31, Application US/09056105

Patent No. 6287569

GENERAL INFORMATION:

APPLICANT: KIPPS, THOMAS J.

APPLICANT: MU, YUNQI

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

```
RESULT 8
US-09-605-785-607
; Sequence 607, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 607
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-605-785-607

Query Match
Best Local Similarity 83.3%; Score 20; DB 4; Length 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGCTT 20
Db 3 ATGTGGTCCCGGTGCTT 22

RESULT 9
US-08-394-033-1
; Sequence 1, Application US/08394033
; Patent No. 5614372
; GENERAL INFORMATION:
; APPLICANT: Lundvall, Hans
; APPLICANT: Lovgren, Janita
; TITLE OF INVENTION: Early Detection of Prostate Cancer (CAP)
; TITLE OF INVENTION: by Employing Prostate Specific Antigen (PSA) and Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, NW, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,033

FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 23635-113884
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-394-033-1

Query Match
Best Local Similarity 75.0%; Score 18; DB 1; Length 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTC 18
Db 11 ATGTGGTCCCGGTGTC 28

RESULT 10
US-08-577-492-31
; Sequence 31, Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784 is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,492
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2153 base pairs
```

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-577-492-31

Query Match 75.0%; Score 18; DB 2; Length 2153;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GGTCCCGGTGCTCTCCT 23
DB 198 GGTCCCGGTGCTCTCCT 215

RESULT 11
US-09-079-630-31
Sequence 31, Application US/09079630
Patent No. 6291199
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
APPLICANT: Lumb, Simon Mark
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199Pis
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 630
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/577,492
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 2153 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-079-630-31

Query Match 75.0%; Score 18; DB 4; Length 2153;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GGTCCCGGTGCTCTCCT 23
DB 198 GGTCCCGGTGCTCTCCT 215

RESULT 12

US-09-042-071-19/C
Sequence 19, Application US/09042071
Patent No. 6294372
GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 660081, 407
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-042-071-19

Query Match 73.3%; Score 17.6; DB 4; Length 1548;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ATGTGGTCCCGGTGCTCTCCTC 24
DB 411 ATGTGGTCCCGGTGCTCTCCTC 388

RESULT 13
US-08-454-720A-38/C
Sequence 38, Application US/08454720A
Patent No. 5766888
GENERAL INFORMATION:
APPLICANT: Sobol, Robert E.
APPLICANT: Green, Mark R.
APPLICANT: Kawasaki, Ernest S.
TITLE OF INVENTION: Detection of Carcinoma Metastases by
TITLE OF INVENTION: Nucleic Acid Amplification
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffman-La Roche, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0L, version

Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rni

Page 6

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,720A
; FILING DATE: May 31, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,565
; FILING DATE: December 16, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas
; REGISTRATION NUMBER: 35321
; REFERENCE/DOCKET NUMBER: 9178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-454-720A-38

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Query Match          68.3%; Score 16.4; DB 1; Length 1864;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 7 GTCCGGTGTCTCTCCTC 24
    |||||
DB 1189 GTCCGGTGTCTCTCCTC 1172

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```

RESULT 14
US-08-983-075D-10
; Sequence 10 Application US/08983075D
; Patent No. 6303361
; GENERAL INFORMATION:
; APPLICANT: VIKKO, Pirkko
; TITLE OF INVENTION: HUMAN GLANDULAR KALLIKREIN-1 (HK2)
; FILE REFERENCE: 1491/44025
; CURRENT APPLICATION NUMBER: US/08/983,075D
; CURRENT FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/FI96/00382
; PRIOR FILING DATE: 1996-06-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: nucleotide sequence encoding the prepro-sequence
; OTHER INFORMATION: of the hk2 protein
US-08-983-075D-10

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Query Match          66.7%; Score 16; DB 4; Length 72;
Best Local Similarity 79.2%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

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OY 1 ATGTGGTCCCGGTGTCTCTCCTC 24
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DB 1 ATGTGGACCTGTCTCTCATC 24

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RESULT 15
US-09-385-982-435/C
; Sequence 435, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II

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; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 435
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-435

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Query Match          66.7%; Score 16; DB 4; Length 558;
Best Local Similarity 79.2%; Pred. No. 1402;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```

OY 1 ATGTGGTCCCGGTGTCTCTCCTC 24
    |||||
DB 237 ATTTGGTCACGCTCTCTCTCCTC 214

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Search completed: November 19, 2002, 05:20:20
Job time : 54.0769 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:04:51 : Search time 81.2308 Seconds
(without alignments)
111.898 Million cell updates/sec

Title: US-09-829-004A-7

Perfect score: 24
Sequence: 1 atgtggccgctgtcttcctc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

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2: /cgn2_6/ptodata/1/pubpna/PCCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCCTUS_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	US-09-829-004A-7	Sequence 7, Appli
2	24	100.0	1709	US-09-755-100-4	Sequence 4, Appli
3	24	100.0	3423	US-09-755-100-5	Sequence 5, Appli
4	24	100.0	3846	US-09-755-100-3	Sequence 3, Appli
5	24	100.0	4661	US-09-755-100-1	Sequence 1, Appli
6	24	100.0	4661	US-09-755-100-2	Sequence 2, Appli
7	20	83.3	22	US-09-755-143-607	Sequence 607, App
8	20	83.3	22	US-09-780-669-607	Sequence 607, App
9	20	83.3	22	US-09-822-827-607	Sequence 607, App
10	19.2	80.0	612	US-09-974-300-2790	Sequence 2790, App
11	16.8	70.0	1484	US-09-764-868-429	Sequence 429, App
12	16.8	70.0	2484	US-09-036-613-4	Sequence 16219, A
13	16.2	67.5	569	US-09-864-761-16219	Sequence 2277, Ap
14	16.2	67.5	975	US-09-938-842A-2277	Sequence 3, Appli
15	16.2	67.5	33239	US-09-814-950-3	Sequence 979, App
16	16.2	67.5	31	US-09-801-274-979	Sequence 20503, A
17	16	66.7	373	US-09-864-761-20503	Sequence 13058, A
18	16	66.7	381	US-09-960-352-13058	Sequence 2854, A
19	16	66.7	393	US-09-960-352-2854	

20	16	66.7	432	10	US-09-960-352-12564	Sequence 12564, A
21	16	66.7	434	10	US-09-960-352-11130	Sequence 11130, A
22	16	66.7	443	10	US-09-960-352-257	Sequence 257, App
23	16	66.7	447	10	US-09-920-300A-335	Sequence 335, App
24	16	66.7	447	12	US-10-033-528-335	Sequence 4335, App
25	16	66.7	450	10	US-09-960-353-4535	Sequence 286, App
26	16	66.7	861	10	US-09-925-297-286	Sequence 7, Appli
27	16	66.7	871	10	US-09-956-999-7	Sequence 101, App
28	16	66.7	871	10	US-09-962-832-101	Sequence 2307, App
29	16	66.7	871	10	US-09-880-107-2307	Sequence 1532, App
30	16	66.7	1144	10	US-09-974-300-1532	Sequence 6, Appli
31	16	66.7	1261	10	US-09-755-100-6	Sequence 1, Appli
32	16	66.7	1500	10	US-09-938-642-1	Sequence 153, App
33	16	66.7	1678	10	US-09-925-300-153	Sequence 348, App
34	16	66.7	2044	10	US-09-925-302-348	Sequence 347, App
35	16	66.7	2169	12	US-10-044-090-347	Sequence 65, Appli
36	15.8	65.8	54	10	US-09-918-063-65	Sequence 67, Appli
37	15.8	65.8	54	10	US-09-918-063-67	Sequence 699, App
38	15.8	65.8	275	10	US-09-777-564-699	Sequence 1235, App
39	15.8	65.8	319	10	US-09-777-564-1235	Sequence 1047, App
40	15.8	65.8	412	9	US-09-736-457-1047	Sequence 14, Appli
41	15.8	65.8	612	10	US-09-918-063-14	Sequence 16, Appli
42	15.8	65.8	612	10	US-09-918-063-16	Sequence 29, Appli
43	15.8	65.8	612	10	US-09-918-063-29	Sequence 31, Appli
44	15.8	65.8	612	10	US-09-918-063-31	Sequence 73, Appli
45	15.8	65.8	681	10	US-09-918-063-73	

ALIGNMENTS

RESULT 1
US-09-829-004A-7
Sequence 7, Application US/09829004A
Patent No. US20020132976A1
GENERAL INFORMATION:
APPLICANT: Chong, Pele
APPLICANT: Pedyczak, Artur
TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Antigen (P
FILE REFERENCE: 11014-24
CURRENT APPLICATION NUMBER: US/09/829,004A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/195,456
PRIOR FILING DATE: 2000-04-10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CLP313
US-09-829-004A-7
Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTCCCGTGTCTTCTC 24
DB 1 ATGTGGTCCCGTGTCTTCTC 24
RESULT 2
US-09-755-100-4
Sequence 4, Application US/09755100
Patent No. US20020099189A1
GENERAL INFORMATION:
APPLICANT: SAVITZKY, Kinnet et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 2786-0156P

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; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-4

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 1709;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGTCTCTC 24
Db 1502 ATGTGGTCCCGGTTGTCTCTC 1525

RESULT 3
US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 3423;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGTCTCTC 24
Db 1502 ATGTGGTCCCGGTTGTCTCTC 1525

RESULT 4
US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL131363
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; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 3846;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGTCTCTC 24
Db 1502 ATGTGGTCCCGGTTGTCTCTC 1525

RESULT 5
US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 4661;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGTCTCTC 24
Db 1502 ATGTGGTCCCGGTTGTCTCTC 1525

RESULT 6
US-09-755-100-2
; Sequence 2, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-755-100-2

Query Match 100.0%; Score 24; DB 10; Length 4661;
Best Local Similarity 100.0%; Pred. No. 0.029; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 ATGTGGGTCCCGGTGTCTCTC 24
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DB 1502 ATGTGGGTCCCGGTGTCTCTC 1525

RESULT 7

US-09-759-143-607
; Sequence 607, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepier, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 607
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-759-143-607

Query Match 83.3%; Score 20; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20
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DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 8

US-09-780-669-607
; Sequence 607, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepier, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 607
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-780-669-607

Query Match 83.3%; Score 20; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20
|||||
DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 9

US-09-822-827-607
; Sequence 607, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 962
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 607
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-822-827-607

Query Match 83.3%; Score 20; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20
|||||
DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 10

US-09-974-300-2790/c
; Sequence 2790, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:

APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2790
LENGTH: 612
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-2790

Query Match 80.0%; Score 19.2; DB 10; Length 612;
Best Local Similarity 87.5%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ATGTGGTCCCGGTGCTCTCC 24
DB 293 ATATCGTCCCGGTGCTCTCC 270

RESULT 11
US-09-764-868-429/C
Sequence 429, Application US/09764868
Patent No. US2002016871A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 429
LENGTH: 1484
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1410)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1418)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-429

Query Match 70.0%; Score 16.8; DB 9; Length 1484;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GTGGGTCCCGGTGCTCTCC 22
DB 467 GTGGGTCCCGGTGCTCTCC 448

RESULT 12
US-09-036-613-4/C
Sequence 4, Application US/09036613
Patent No. US2002015135A1
GENERAL INFORMATION:
APPLICANT: Yue, Henry

APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: SYNAPSE RELATED GLYCO PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,613
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0488 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
FAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOS12
CLONE: 2762136
US-09-036-613-4

Query Match 70.0%; Score 16.8; DB 10; Length 2484;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GTGGGTCCCGGTGCTCTCC 22
DB 586 GTGGGTCCCGGTGCTCTCC 567

RESULT 13
US-09-864-761-16219
Sequence 16219, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16219
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007539.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
US-09-864-761-16219
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Query Match          67.5%; Score 16.2; DB 10; Length 569;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 3 GTGGGTCCCGGTTGCTTCCT 23
Db 455 GTGGGGCCAGGTGTCTCCTC 475
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RESULT 14
US-09-938-842A-2277/c
; Sequence 2277, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRRP1300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2277
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2277
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Query Match          67.5%; Score 16.2; DB 9; Length 975;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 4 TGGGTCCCGGTTGCTTCCTC 24
Db 343 TGGATCCCGGCTGCTTCCTC 323
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RESULT 15
US-09-814-950-3
; Sequence 3, Application US/09814950
; Patent No. US20020137130A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 33239
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(33239)
; OTHER INFORMATION: n = A,T,C or G
US-09-814-950-3
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```

Query Match          67.5%; Score 16.2; DB 10; Length 33239;
Best Local Similarity 85.7%; Pred. No. 14e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 2 TGTGGTCCCGGTTGCTTCCTC 22
Db 27025 TGTGGTCCAGGTGCTTCCTC 27045
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 00:33:44 ; Search time 1026.35 Seconds

(without alignments)
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Title: US-09-829-004a-8

Perfect score: 27
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum Match 100%
Listing first 45 summaries

Database :

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32: em_hgt_other: *
33: em_hgt_mus: *
34: em_hgt_pln: *
35: em_hgt_rod: *
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37: em_hgt_vrt: *
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39: em_hgt_hum: *
40: em_hgt_mus: *
41: em_hgt_other: *

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score greater than or equal to the score of the result being printed,
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	6 AX281251	AX281251 Sequence
2	27	100.0	200	6 AR047835	AR047835 Sequence
3	27	100.0	287	9 HSPSA2	X13941 Human PSA g
4	27	100.0	569	9 S75755	S75755 PSA-Prostat
5	27	100.0	658	9 HUMPA2	M21897 Human Prost
6	27	100.0	708	9 HSA310937	AR153342 Sequence
7	27	100.0	711	6 AR153342	AR153342 Sequence
8	27	100.0	711	6 BD007601	BD007601 Method to
9	27	100.0	870	9 HSA459783	AJ459783 Homo sapi
10	27	100.0	876	9 HSA459782	AJ459782 Homo sapi
11	27	100.0	990	9 HSU17040	U17040 Human prost
12	27	100.0	992	6 I67863	I67863 Sequence 13
13	27	100.0	1130	9 AF335477	AF335477 Homo sapi
14	27	100.0	1350	6 AX200986	AX200986 Sequence
15	27	100.0	1350	6 AX267642	AX267642 Sequence
16	27	100.0	1415	9 HUMPA3	M21895 Human prost
17	27	100.0	1446	9 HUMAPS	M26653 Homo sapien
18	27	100.0	1462	6 I67864	I67864 Sequence 14
19	27	100.0	1466	6 E32812	E32812 Primer DNA
20	27	100.0	1466	9 HSPSAR	X05332 Human mRNA
21	27	100.0	1492	9 BC005307	BC005307 Homo sapi
22	27	100.0	1514	9 MPMROS	X73560 M.mutata m
23	27	100.0	1603	9 HSA310938	AJ310938 Homo sapi
24	27	100.0	1654	9 HUMPA3	M21896 Human prost
25	27	100.0	1729	6 AR059540	AR059540 Sequence
26	27	100.0	1729	6 AR082934	AR082934 Sequence
27	27	100.0	1729	6 AX337560	AX337560 Sequence
28	27	100.0	1729	9 HSPSA	X07730 Human mRNA
29	27	100.0	1945	9 AF335478	AF335478 Homo sapi
30	27	100.0	2106	6 AX106218	AX106218 Sequence
31	27	100.0	3423	6 AX033404	AX033404 Sequence
32	27	100.0	3846	6 AX033402	AX033402 Sequence
33	27	100.0	4661	6 AX033400	AX033400 Sequence
34	27	100.0	4661	6 AX033401	AX033401 Sequence
35	27	100.0	5873	9 HSPSAG	X14810 Human DNA f
36	27	100.0	6153	9 HUMPSANTIG	M24543 Human prost
37	27	100.0	7130	6 A37262	A37262 Sequence 2
38	27	100.0	7130	6 AR167395	AR167395 Sequence
39	27	100.0	7130	9 HUMPSAA	M27274 Human prost
40	27	100.0	40458	9 AC011523	AC011523 Homo sapi
41	27	100.0	217346	2 AC027602	AC027602 Homo sapi
42	27	100.0	230000	9 AF243527	AF243527 Homo sapi
43	23.8	88.1	711	6 AR105688	AR105688 Sequence
44	23.8	88.1	711	6 AR105695	AR105695 Sequence
45	23.8	88.1	711	6 AR153341	AR153341 Sequence

ALIGNMENTS

RESULT 1
AX281251
LOCUS
DEFINITION Sequence 8 from Patent WO0176622.
ACCESSION AX281251
VERSION AX281251.1 GI:16608507
KEYWORDS
ORGANISM
SOURCE
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE
1 Pedyczak A., Chong P. and Sia C.D.
TITLE Immunogenic peptides derived from prostate-specific antigen (psa)
and uses thereof
JOURNAL Patent: WO 0176622-A 8 18-OCt-2001;

Avantis Pasteur Limited (CA)
Location/Qualifiers
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="CIP314"

BASE COUNT 2 a 10 c 8 g 7 t

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 1 GTTCTGTGACCCCGAGTGGTCTC 27

RESULT 2
LOCUS AR047835 200 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5817798;
ACCESSION AR047835
VERSION AR047835.1 GI:5969300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 200)
AUTHORS Gundling, G. J.
TITLE Rapid RNA isolation procedure in the presence of a transition metal ion
JOURNAL Patent: US 5817798-A 1 06-OCT-1998;
FEATURES
Location/Qualifiers
1..200
BASE COUNT 31 a 58 c 67 g 44 t

Query Match 100.0%; Score 27; DB 6; Length 200;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 120 GTTCTGTGACCCCGAGTGGTCTC 146

RESULT 3
LOCUS HSPSA2 287 bp DNA linear PRI 24-AUG-1989
DEFINITION Human PSA gene for prostate specific antigen exon 2.
ACCESSION X13941.1 GI:35724
VERSION X13941.1 GI:35724
KEYWORDS Kallikrein; prostate specific antigen; PSA gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 287)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-1989) Digby M.R., The Howard Florey Institute, Melbourne University, Parkville, Victoria 3052, Australia
REFERENCE 2 (bases 1 to 287)
AUTHORS Digby, M., Zhang, X.Y. and Richards, R.I.
TITLE Human prostate specific antigen (PSA) gene: structure and linkage to the kallikrein-like gene, hK1
JOURNAL Nucleic Acids Res. 17 (5), 2137 (1989)
MEDLINE 89183632
JOURNAL 2467258
COMMENT Data kindly reviewed (16-may-1989) by Digby M.R.
FEATURES Location/Qualifiers

source
1..287
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="Chromosome 19"
/clone="CHK-2"
/clone_lib="cosmid"
1..107
/note="intron 1"
108..267
/note="exon 2"
108..267
/note="prostate specific antigen (AA 16-69) (108 is 2nd base in codon) (267 is 2nd base in codon); Protein sequence is in conflict with the conceptual translation"
/codon_start=1
/protein_id="CAA32124.1"
/db_xref="GI:1335282"
/db_xref="SWISS-PROT:P07288"
/translation="ALRPSGLGLMEAGSARISIPNRCILPLVAGQSAAYFWCTPSG SOLTPASG"
268..>287
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43 a 100 c 78 g 66 t

BASE COUNT 43 a 100 c 78 g 66 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 287;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 218 GTTCTGTGACCCCGAGTGGTCTC 244

RESULT 4
LOCUS S75755 569 bp mRNA linear PRI 15-JUN-1995
DEFINITION PSA-prostate-specific antigen [human, breast cancer specimen, mRNA Partial, 569 nt].
ACCESSION S75755.1 GI:861469
VERSION S75755.1 GI:861469
KEYWORDS
SOURCE Homo sapiens breast cancer specimen.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 569)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Molecular characterization of prostate-specific antigen messenger RNA expressed in breast tumors
JOURNAL Cancer Res. 54 (24), 6344-6347 (1994)
MEDLINE 95079406
JOURNAL 7527295
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1b5q 161505] from the original journal article.
FEATURES
Location/Qualifiers
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..569
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/gene="PSA"
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1..569
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/note="prostate-specific antigen"
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/note="prostate-specific antigen"
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/db_xref="GI:4261885"
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BASE COUNT 108 a 182 c 160 g 119 t
ORIGIN LGTTCYASGWSIEPEEFLTPKKLOCVLD,
Query Match 100.0%; Score 27; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTCTGTGTCACCCAGTGGTCTC 27
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Db 198 GTTCTGTGTCACCCAGTGGTCTC 224
|||||
RESULT 5
LOCUS HUMPA6 658 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human prostate specific antigen (Pa) gene, 3' end, clone PA 424.
ACCESSION M21897
VERSION M21897.1 GI:189529
KEYWORDS glycoprotein; prostate antigen; prostate-specific antigen;
semioangelin.
SOURCE Human prostate tumor cell line PC 82, CDNA to mRNA, clone PA 424.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Riegman,P.H., Klaassen,P., van der Korp,J.A., Romijn,J.C. and
Trapman,J.
TITLE Molecular cloning and characterization of novel prostate antigen
CDNA's
JOURNAL Biochem. Biophys. Res. Commun. 155 (1), 181-188 (1988)
MEDLINE 8836297
PUBMED 2458104
FEATURES
source location/Qualifiers
1..658
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19q13.3"
1..658
/gene="APS"
/gene="APS"
/gene="APS"
/note="prostate specific antigen precursor"
/codon_start=2
/protein_id="AA59997.1"
/db_xref="GI:189530"
/db_xref="GDB:G00-119-695"
/translation="VVFILSVTWIGAAPLISRIYGVGNECKHSQPMQVLAASRGRA
VCGVYLHPQWVLTAAHCIRNKSIVILGRHSILFHPEDTGOVQVSHSPHPPLDMSLL
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CTPPDGAAGSPDAMV"
<1..40
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/gene="APS"
/note="prostate specific antigen signal peptide"
62..559
/gene="APS"
/note="prostate specific antigen"
BASE COUNT 125 a 195 c 206 g 132 t
ORIGIN 176 bp upstream of PvuII site.
Query Match 100.0%; Score 27; DB 9; Length 658;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTCTGTGTCACCCAGTGGTCTC 27
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Db 146 GTTCTGTGTCACCCAGTGGTCTC 172
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RESULT 6
LOCUS HSAJ10937 708 bp mRNA linear PRI 17-JAN-2002
DEFINITION Homo sapiens mRNA for putative preproPSA-RP2 (KLK3 gene),
transcript 1.
AJ310937
VERSION AJ310937.1 GI:14422304
KEYWORDS alternative splicing; HKLK3 gene; kallikrein 3; preproPSA-RP2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Heuze-Vourc'h,N., Leblond,V., Olayat,S., Gauthier,F. and Courty,Y.
TITLE Characterization of PSA-RP2, a protein related to prostate-specific
antigen and encoded by alternative HKLK3 transcripts
Eur J. Biochem. 268 (16), 4408-4413 (2001)
JOURNAL MEDLINE 21393944
PUBMED 11502200
REFERENCE 2 (bases 1 to 708)
AUTHORS Courty,Y.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2001) Courty Y., Faculte de Medecine, EMI-U 0010,
laboratoire d'Enzymologie, 2 bis bd Tonnelie, 37032 Tours cedex,
FRANCE
COMMENT related accession number AJ310938;
FEATURES
source location/Qualifiers
1..708
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NH101007.97"
/cell_line="LNCap"
1..708
/gene="KLK3"
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38..580
/gene="KLK3"
/function="unknown"
/note="alternative splicing, transcript 1"
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/translation="MWVVFILSVTWIGAAPLISRIYGVGNECKHSQPMQVLAAS
RGRAVCGVYLHPQWVLTAAHCIRNKSIVILGRHSILFHPEDTGOVQVSHSPHPPLD
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38..88
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110..577
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578..708
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/gene="KLK3"
/evidence="experimental"
BASE COUNT 134 a 214 c 219 g 141 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 708;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTCTGTGTCACCCAGTGGTCTC 27
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Db 194 GTTCTGTGTCACCCAGTGGTCTC 220
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RESULT 7
LOCUS AR153342 711 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6235486.
ACCESSION AR153342
VERSION AR153342.1 GI:15120874
KEYWORDS

transcript 1.
AJ310937
VERSION AJ310937.1 GI:14422304
KEYWORDS alternative splicing; HKLK3 gene; kallikrein 3; preproPSA-RP2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Heuze-Vourc'h,N., Leblond,V., Olayat,S., Gauthier,F. and Courty,Y.
TITLE Characterization of PSA-RP2, a protein related to prostate-specific
antigen and encoded by alternative HKLK3 transcripts
Eur J. Biochem. 268 (16), 4408-4413 (2001)
JOURNAL MEDLINE 21393944
PUBMED 11502200
REFERENCE 2 (bases 1 to 708)
AUTHORS Courty,Y.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2001) Courty Y., Faculte de Medecine, EMI-U 0010,
laboratoire d'Enzymologie, 2 bis bd Tonnelie, 37032 Tours cedex,
FRANCE
COMMENT related accession number AJ310938;
FEATURES
source location/Qualifiers
1..708
/organism="Homo sapiens"
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38..580
/gene="KLK3"
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/note="alternative splicing, transcript 1"
/codon_start=1
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/db_xref="GI:14422305"
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RGRAVCGVYLHPQWVLTAAHCIRNKSIVILGRHSILFHPEDTGOVQVSHSPHPPLD
MSLLKNRFLRPDSSHDMLRLSEPAELTAVKVDPTQEPALGTTTCYASGWSIE
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38..88
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578..708
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708
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/gene="KLK3"
/evidence="experimental"
BASE COUNT 134 a 214 c 219 g 141 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 708;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTCTGTGTCACCCAGTGGTCTC 27
|||||
Db 194 GTTCTGTGTCACCCAGTGGTCTC 220
|||||
RESULT 7
LOCUS AR153342 711 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6235486.
ACCESSION AR153342
VERSION AR153342.1 GI:15120874
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 711)
AUTHORS      Young,C.Y.F., Tindall,D.J. and Klee,G.G.
TITLE        Method for detection of breast cancer
JOURNAL      Patent: US 623486-A 4 22-MAY-2001;
FEATURES     Location/Qualifiers
             source          1..711
             /organism="unknown"
BASE COUNT   148 a 208 c 206 g 149 t
ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGCTCTC 27
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Db 85 GTTCTGTGACACCCAGTGGCTCTC 111

RESULT 8
LOCUS        BD007601 711 bp DNA linear PAT 31-JAN-2002
DEFINITION   Method for detecting metastatic prostatic cancer.
ACCESSION    BD007601
VERSION      BD007601.1 GI:18635974
KEYWORDS     JP 2001503991-A/14.
SOURCE       unidentified.
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 711)
AUTHORS      Tindall,D.J., Young,C.Y.F., McCormic,D.J., Klee,G.G., Saeedi,M.S.,
              Kumar,A., Rittenhouse,H.G. and Wolfert,R.L.
TITLE        Method for detecting metastatic prostatic cancer
JOURNAL      Patent: JP 2001503991-A 14 27-MAR-2001;
COMMENT      MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH, HYBRITTECH INC
FEATURES     Location/Qualifiers
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             /db_xref="taxon:32644"
BASE COUNT   148 a 208 c 206 g 149 t
ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGCTCTC 27
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Db 85 GTTCTGTGACACCCAGTGGCTCTC 111

RESULT 9
HSA459783

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LOCUS        HSA459783 870 bp mRNA linear PRI 09-MAY-2002
DEFINITION   Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice
              variant 2.
ACCESSION    AJ459783
VERSION      AJ459783.1 GI:20520642
KEYWORDS     alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    Heuze-Vourc'h,N. and Courty,Y.
              Complex alternative splicing of the hKLK3 gene coding for the
              tumour marker PSA (prostate-specific-antigen)
              unpublished
              2 (bases 1 to 870)
REFERENCE    Direct Submission
              Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire
              d'enzymologie, Universite F. Rabatelais, 2 bis bvd Tonnelier, Tours,
              37032 cedex FRANCE
              alternative splice variant sequences: AJ459782, AJ459784.
FEATURES     Location/Qualifiers
             source          1..870
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="YC140405-00"
             /tissue_type="prostate"
             1..870
             /gene="KLK3"
             22..807
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             /codon_start=1
             /evidence=experimental
             /product="prostate specific antigen"
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             /db_xref="GI:20520643"
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              MSLKRFELRPDDSSHDLMILRSEPEFLIDAKYWDIPROPALACTGCGXSGMSI
              EPERFLPKQLQCVLDHVISNDVCAQVPHQVTKMCAQRMFGSGTSGSDSGPFLV
              CNGVLOGTISWSEPCALPERPSLTKVHVTKMKDKITVAMP
              22..72
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              /product="prostate specific antigen"
BASE COUNT   185 a 257 c 242 g 186 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGCTCTC 27
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Db 178 GTTCTGTGACACCCAGTGGCTCTC 204

RESULT 10
HSA459782 876 bp mRNA linear PRI 09-MAY-2002
LOCUS        HSA459782
DEFINITION   Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice
              variant 1.
ACCESSION    AJ459782
VERSION      AJ459782.1 GI:20520640
KEYWORDS     alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1

```


AUTHORS Heuze-Yourc'h, N. and Court'y, Y.
TITLE Complex alternative splicing of the hKlk3 gene coding for the
tumor marker PSA (prostate specific-antigen)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 876)
AUTHORS Court'y, Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Court'y Y., EMI-U 0010, Laboratoire
d'Enzymologie, Universite F. Rabelaais, 2 bis bvd Tonnelie, Tours,
37032 cedex, FRANCE
COMMENT alternative splice variant sequences: A4459783, A4459784.
FEATURES
source
1..876
/organism="Homo sapiens"
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/clone="YC111105-00"
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22..684
/gene="KLK3"
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/codon_start=1
/evidence="experimental"
/product="prostate specific antigen"
/protein_id="CAD30844.1"
/db_xref="GI:20520641"
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MSLKNRFLRPDDSDSIEPEEFLTPKLCQVDLHVISNDVCAQVHPQVTKRMLCAGR
WTGKSTCSGDSGGLVPCNGVLOGITSMGSEPCALPERPSLYTKVHYHKKWIKDTIVANP"
sig_peptide 22..72
/gene="KLK3"
94..681
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/product="prostate specific antigen"
235 c 231 g 190 t
BASE COUNT 220 a
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Query Match 100.0%; Score 27; DB 9; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 178 GTTCTGTGACCCCGAGTGGTCTC 204
RESULT 11
LOCUS HSU17040 990 bp mRNA linear PRI 07-DEC-1994
DEFINITION Human prostate specific antigen precursor mRNA, complete cds.
ACCESSION U17040
VERSION U17040.1 GI:595945
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 990)
AUTHORS Monne, M.M., Moreno, J.M., Mele, C.M., Mulholland, G.M. and
Gomella, L.G.
TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence
JOURNAL In Benign and Malignant Prostate Tissue
REFERENCE Unpublished
AUTHORS Moreno, J.M.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1994) Jose M J G Moreno, Urology, Thomas
Jefferson University Hospital, 1025 Walnut Street, Philadelphia, PA
19107, USA
FEATURES Location/Qualifiers

source
1..990
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/sex="male"
/tissue_type="prostate"
42..827
/codon_start=1
/product="prostate specific antigen precursor"
/protein_id="AAA56764.1"
/db_xref="GI:595946"
/translation="MMVPVFLTSLVTWGAAPLILSRIVGMECEKHSOPMOVLVAS
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MSLKNRFLRPDDSDSMDLRLRSEPAELTAVVYMDLPTPEPALGTTTCVSGMGSI
EPEEFLTPKLCQVDLHVISNDVCAQVHPQVTKRMLCAGRTGKSTCSGDSGGLV
CNGVLOGITSMGSEPCALPERPSLYTKVHYHKKWIKDTIVANP"
sig_peptide 42..92
mat_peptide 114..824
misc_feature 93..113
/note="propeptide"
BASE COUNT 209 a 291 c 273 g 217 t
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Query Match 100.0%; Score 27; DB 9; Length 990;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 198 GTTCTGTGACCCCGAGTGGTCTC 224
RESULT 12
LOCUS I67863 992 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 13 from patent US 5674682.
ACCESSION I67863
VERSION I67863.1 GI:2829985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 992)
AUTHORS Croce, C., Gomella, L., Mulholland, S., Grant, J., Moreno, J.G. and
Fischer, R.
TITLE Nucleic acid primers for detecting micrometastasis of prostate
cancer
JOURNAL Patent: US 5674682-A 13 07-OCT-1997;
FEATURES Location/Qualifiers
source
1..992
/organism="unknown"
BASE COUNT 210 a 291 c 272 g 217 t 2 others
ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 992;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGACCCCGAGTGGTCTC 27
Db 200 GTTCTGTGACCCCGAGTGGTCTC 226
RESULT 13
LOCUS AF335477 1130 bp mRNA linear PRI 13-MAY-2002
DEFINITION Homo sapiens prostate-specific antigen variant 1 mRNA, complete
ACCESSION AF335477
VERSION AF335477.1 GI:18478569
KEYWORDS

SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1130)
David, A., Mable, N., Azar, I., Bilton, S., Engel, S., Bernstein, J., Romano, J., Avigor, Y., Waks, T., Eshhar, Z., Langer, S.Z., Lifschitz-Mercer, B., Matzkin, H., Rotman, G., Toporik, A., Savitsky, K. and Mintz, L.
TITLE Unusual alternative splicing within the human kallikrein genes KLK2 and KLK3 gives rise to novel prostate-specific proteins
JOURNAL J. Biol. Chem. 277 (20), 18084-18090 (2002)
MEDLINE 22001285
PUBMED 11834722
AUTHORS 2 (bases 1 to 1130)
David, A., Engel, S., Azar, I., Bernstein, J., Rotman, G., Savitsky, K. and Mintz, L.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Compugen Ltd., 72 Pinchas Rosen, Tel Aviv 69512, Israel
FEATURES
Source Location/Qualifiers
1..1130
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
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42..356
/note="PSA; KLK3; alternatively spliced"
/codon_start=1
/product="prostate-specific antigen variant 1"
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/db_xref="GI:18478570"
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PSPREHGSFLPAPLQAHNTSPSILQOSSPHQVPAPSHLPQNFPIQAPACQL
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BASE COUNT 213 a 374 c 291 g 252 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTCACCCCGAGTGGTCTC 27
DB 621 GTTCTGTCACCCCGAGTGGTCTC 647
RESULT 14
AX200986 1350 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 616 from Patent W00151633.
DEFINITION AX200986
ACCESSION AX200986
VERSION AX200986.1 GI:15390813
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1350)
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skelky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0151633-A 616 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Source Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 778 GTTCTGTCACCCCGAGTGGTCTC 804
Search completed: November 19, 2002, 04:02:54
Job time : 1028.66 secs

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 778 GTTCTGTCACCCCGAGTGGTCTC 804
RESULT 15
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LOCUS Sequence 616 from Patent W00173032.
DEFINITION AX267642
ACCESSION AX267642
VERSION AX267642.1 GI:16516315
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0173032-A 616 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
Source Location/Qualifiers
1..1350
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 284 a 404 c 391 g 271 t
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Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 778 GTTCTGTCACCCCGAGTGGTCTC 804
Search completed: November 19, 2002, 04:02:54
Job time : 1028.66 secs

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OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 23:02:59 : Search time 191.769 Seconds
(without alignments)
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Title: US-09-829-004A-8
Perfect score: 27
Sequence: 1 gtctgtgtcacccagtggtctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	22	AAD21362
2	27	100.0	178	24	ABA92483
3	27	100.0	178	24	ABA01120
4	27	100.0	200	19	AAV60379
5	27	100.0	208	18	AAT92975
6	27	100.0	517	21	AAA61482
7	27	100.0	517	21	AAH41845
8	27	100.0	711	20	AAK08947
9	27	100.0	744	24	ABK86205

10	27	100.0	841	23	ABV25078	Human prostate exp
11	27	100.0	990	21	AA247134	Human prostate-spe
12	27	100.0	992	18	AAT91054	Human prostate spe
13	27	100.0	992	20	AAK99846	Prostate specific
14	27	100.0	1040	22	AAH99720	Human prostate enco
15	27	100.0	1066	21	AAC03740	Human secreted pro
16	27	100.0	1329	23	ABV23473	Human prostate exp
17	27	100.0	1329	23	ABV29201	Human prostate exp
18	27	100.0	1350	22	AAK56394	Human prostate exp
19	27	100.0	1350	22	AAH93860	Human CDNA encodin
20	27	100.0	1350	24	ABU93534	P703P and PSA fusi
21	27	100.0	1445	19	AAV32497	Human P703P/PSA fu
22	27	100.0	1462	18	AAT91055	Prostate specific
23	27	100.0	1462	18	AAV98477	Human prostate spe
24	27	100.0	1466	19	AAV32496	Prostate specific
25	27	100.0	1466	21	AAH17111	Prostate specific
26	27	100.0	1728	17	AAT35867	Human prostate-spe
27	27	100.0	1729	16	AAT04864	Prostate-specific
28	27	100.0	1729	24	ABL69732	Prostate cancer re
29	27	100.0	2106	22	AAK69658	Human WT1/PSA fusi
30	27	100.0	3423	21	AAA64171	DNA encoding a hum
31	27	100.0	3846	21	AAH64169	DNA encoding a hum
32	27	100.0	4661	21	AAA64167	DNA encoding a hum
33	27	100.0	4661	21	AAA64168	DNA encoding a hum
34	27	100.0	5873	18	AAT61701	Human prostatic sp
35	25.4	94.1	1866	23	ABV23503	Human prostate exp
36	25.4	94.1	1866	23	ABV24768	Human prostate exp
37	25.4	94.1	1866	23	ABV29105	Human prostate exp
38	25.4	94.1	1866	23	ABV29331	Human prostate exp
39	24.4	90.4	151	23	ABV38196	Human prostate exp
40	23.8	88.1	163	23	ABV37921	Human prostate exp
41	23.8	88.1	233	23	ABV45098	Human prostate exp
42	23.8	88.1	275	21	AAC72139	Single nucleotide
43	23.8	88.1	385	21	AAK04575	Human secreted pro
44	23.8	88.1	441	23	ABV15240	Human prostate exp
45	23.8	88.1	711	19	AAV70339	Prostate-specific

ALIGNMENTS

RESULT 1	
ID	AAD21362 standard: DNA; 27 BP.
AC	AAD21362;
XX	
AC	28-JAN-2002 (first entry)
DT	
XX	
DE	Prostate specific antigen (PSA) derived peptide, CLP314 encoding DNA.
XX	
KW	Prostate-specific antigen; PSA; immunogenic peptide; immune response;
KW	therapy; cancer; prostate cancer; tumour metastasis; prophyllaxis; ds.
XX	
OS	Unidentified.
XX	
FH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..27
FT	/*tag-a
FT	/product= "PSA derived peptide, CLP314"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	
PN	WO200176622-A2.
XX	
PD	18-OCT-2001.
XX	
PF	10-APR-2001; 2001WO-CA00473.
XX	
PR	10-APR-2000; 2000US-195456P.
XX	
PA	(AVENT) AVENTIS PASTEUR LTD.
XX	

PI Pedyczak A, Chong P, Sia CDY;
 XX WPI: 2001-663015/76.
 DR P-PSDB: AAE13024.
 XX
 XX New polypeptide, useful for treating cancers such as prostate cancer,
 PT comprises prostate-specific antigen derived peptide -
 PS Claim 7, Page 28; 41pp; English.
 XX
 CC The patent discloses immunogenic peptides of prostate-specific antigen
 CC (PSA) and nucleic acids encoding them. The peptides of the invention
 CC are used to prepare a medicament to elicit an immune response in an
 CC animal. They are used to treat cancer such as prostate cancer and
 CC tumour metastasis. They are also useful for prophylaxis, for
 CC preparing monoclonal or polyclonal antibodies, and in conventional
 CC techniques of immunology, molecular biology, cell biology and
 CC recombinant DNA technology. The present sequence is a DNA encoding
 CC PSA derived peptide, CLP314.
 XX
 SQ Sequence 27 BP; 2 A; 10 C; 8 G; 7 T; 0 other;
 Query Match 100.0%; Score 27; DB:22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.023; 0; Mismatches 0; Gaps 0;
 Matches 27; Conservative 0; Indels 0; Gaps 0;
 OY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
 DB 1 GTTCTGTGCACCCCGAGTGGTCTC 27
 RESULT 2
 ABA92483
 ID ABA92483 standard; DNA; 178 BP.
 XX
 AC ABA92483;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE DNA oligonucleotide sequence SEQ ID NO:6.
 XX
 KM Detection; nucleic acid synthesis; identification; cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200183817-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 25-APR-2001; 2001WO-JP03572.
 XX
 PR 01-MAY-2000; 2000JP-0132667.
 XX
 PA (EIKE) EIKEN KAGAKU KK.
 XX
 PI Mori Y, Nagamine K;
 XX
 DR WPI: 2002-075170/10.
 XX
 PT Detecting the product of an enzyme-based nucleic acid synthesizing
 PT reaction, useful in gene analysis, diagnosis of cancer and other
 PT diseases, and in identifying bacteria, comprises the formation of an
 PT insoluble substance -
 PS Example 4; Page 18; 44pp; Japanese.
 XX
 CC The present invention describes a method for detecting the occurrence of
 CC a nucleic acid synthesizing reaction during the synthesis of a nucleic
 CC acid with an enzyme. The method comprises the use of an insoluble
 CC substance formed in the reaction as an indication. The method can be
 CC used for detecting the presence or absence of a nucleic acid synthesizing
 CC reaction (especially a nucleic acid amplification reaction). The method
 CC is useful in gene analysis, diagnosis of cancer and other diseases, and

CC in identifying bacteria. The present sequence represents an
 CC oligonucleotide used in the exemplification of the present invention.
 XX
 SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 other;
 Query Match 100.0%; Score 27; DB:24; Length 178;
 Best Local Similarity 100.0%; Pred. No. 0.034; 0; Mismatches 0;
 Matches 27; Conservative 0; Indels 0; Gaps 0;
 OY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
 DB 39 GTTCTGTGCACCCCGAGTGGTCTC 65
 RESULT 3
 ABA01120
 ID ABA01120 standard; DNA; 178 BP.
 XX
 AC ABA01120;
 XX
 DT 06-FEB-2002 (first entry)
 XX
 DE Human PSA nucleotide sequence.
 XX
 KM Human; nucleic acid synthesis; complementary chain synthesis; diagnosis;
 KM ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200177317-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-JP02771.
 XX
 PR 07-APR-2000; 2000JP-0111939.
 XX
 PA (EIKE) EIKEN KAGAKU KK.
 XX
 PI Notomi T, Nagamine K;
 XX
 DR WPI: 2002-010907/01.
 XX
 PT Isothermal amplification of nucleic acids using double-stranded nucleic
 PT acid as template to establish complementary chain synthesis reaction
 PT from primer enabling base pairing in domain to be annealed, useful e.g.
 PT in gene diagnosis -
 PS Example 1; Page 63; 75pp; Japanese.
 XX
 CC The invention relates to a method for synthesizing a nucleic acid using
 CC a double-stranded nucleic acid as template and incubating under
 CC conditions allowing the establishment of a complementary chain synthesis
 CC reaction. The method uses an arbitrary primer to initiate the
 CC complementary chain synthesis reaction. The method is particularly
 CC useful in gene and disease diagnosis. It is a highly efficient and
 CC reaction specific method in which no temperature variation is required.
 CC The present sequence is used in an example illustrating the invention.
 XX
 SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 other;
 Query Match 100.0%; Score 27; DB:24; Length 178;
 Best Local Similarity 100.0%; Pred. No. 0.034; 0; Mismatches 0;
 Matches 27; Conservative 0; Indels 0; Gaps 0;
 OY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
 DB 39 GTTCTGTGCACCCCGAGTGGTCTC 65
 RESULT 4
 AAV60379
 ID AAV60379 standard; mRNA; 200 BP.

```
XX AC AAV60379;
XX XX
XX DT 07-DEC-1998 (first entry)
XX DE mRNA target sequence from exons 2 and 3 of PSA gene.
XX XX
XX KM mRNA target sequence; prostate specific antigen; PSA; RNA purification;
XX ds.
XX OS Homo sapiens.
XX PN US5817798-A.
XX PD 06-OCT-1998.
XX PF 17-SEP-1997; 97US-0931981.
XX PR 17-SEP-1997; 97US-0931981.
XX PA (ABBO ) ABBOTT LAB.
XX PI Gundling GJ;
XX DR WPI; 1998-556473/47.
XX PT Purification of RNA, used for nucleic acid amplification and disease
XX detection - by precipitating other sample components with transition
XX metal ions, separating and collecting the purified RNA
XX PS Example 5; Columns 9-10; 6pp; English.
XX CC The present sequence represents a mRNA target sequence from exons 2 and 3
XX of the prostate specific antigen (PSA) gene. The sequence is used to
XX exemplify the invention. The specification describes a method for
XX purifying RNA. The method comprises contacting a test sample with
XX polyclonal transition metal ions to form a precipitant and a supernatant,
XX separating the precipitant from the supernatant, and collecting the
XX supernatant to obtain a purified solution of total RNA. The RNA is
XX used for nucleic acid amplification and disease detection.
XX SQ Sequence 200 BP; 31 A; 58 C; 67 G; 44 T; 0 other;
XX
XX Query Match 100.0%; Score 27; DB 19; Length 200;
XX Best Local Similarity 100.0%; Pred. No. 0.035;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCTGTCACCCCGAGTGGTCTC 27
XX |||||||||||||||||||
XX DB 120 GTTCTGTCACCCCGAGTGGTCTC 146
XX
XX RESULT 5
XX AAT92975
XX ID AAT92975 standard; cDNA; 208 BP.
XX XX
XX AC AAT92975;
XX XX
XX DT 24-APR-1998 (first entry)
XX DE cDNA for prostate specific antigen (PSA).
XX XX
XX KM Diagnosis; prostate cancer; prostate specific antigen; PSA;
XX metastatic prostate cancer; prostate cell; secondary tumour;
XX bone metastatic anchoring; ss.
XX OS Homo sapiens.
XX PN WO9739139-A1.
XX PD 23-OCT-1997.
XX PF 16-APR-1997; 97WO-US06497.
```

```
XX PR 16-APR-1996; 96US-0015765.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Robbins DJ;
XX DR WPI; 1997-526473/48.
XX PT Monitoring or diagnosis of prostate cancer - by detecting
XX prostate-specific antigen mRNA using specific primers
XX PS Disclosure; Page 16; 25pp; English.
XX CC cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
XX The detection of PSA mRNA in peripheral blood is associated with
XX metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
XX indicates that prostate cells are circulating in the blood and confirms
XX diagnosis of cancer. Circulating prostate cells also indicate a risk of a
XX secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
XX after prostatectomy or radiotherapy indicates a risk that the prostate
XX cancer has spread and that the surgery and radiotherapy was not
XX effective. PCR primers AAT92971-73 were used for the monitoring and
XX diagnosis of patients with prostate cancer. The method comprises the
XX detection of PSA mRNA by reverse transcriptase polymerase chain reaction
XX (RT-PCR).
XX SQ Sequence 208 BP; 29 A; 62 C; 73 G; 44 T; 0 other;
XX
XX Query Match 100.0%; Score 27; DB 18; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 0.035;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCTGTCACCCCGAGTGGTCTC 27
XX |||||||||||||||||||
XX DB 133 GTTCTGTCACCCCGAGTGGTCTC 159
XX
XX RESULT 6
XX AAA61482
XX ID AAA61482 standard; DNA; 517 BP.
XX XX
XX AC AAA61482;
XX XX
XX DT 23-OCT-2000 (first entry)
XX DE Prostate specific antigen gene fragment.
XX XX
XX KM Isothermal DNA amplification; nucleic acid synthesis; detection;
XX PSA gene template; prostate specific antigen; human; ds.
XX OS Homo sapiens.
XX PN WO200028082-A1.
XX PD 18-MAY-2000.
XX PF 08-NOV-1999; 99WO-JP06213.
XX PR 09-NOV-1998; 98JP-0317476.
XX PA (EIKE ) EIKEN KAGAKU KK.
XX PI Notomi T, Hase T;
XX DR WPI; 2000-376587/32.
XX PT Nucleic acid synthesis using primer containing a sequence identical to
XX one on the template for isothermal amplification using simple reagents
XX Example 8; Fig 17; 95pp; Japanese.
```

CC The invention relates to a novel method of isothermal DNA amplification.
 CC A region is produced at the 3' end of a target sequence which contains
 CC sub-sequences designated F1, F2C and F1C, where F1C is the complement of
 CC F1. A loop is formed by annealing of F1 to its complementary sequence
 CC F1C, and a primer containing a sub-sequence F2 (complementary to F2C) at
 CC its 3' end is annealed to the template. The complementary strand to the
 CC template is synthesized using a DNA polymerase, and the process is
 CC repeated using sub-sequences at the 3' end of the complementary strand
 CC designated R1, R2C and R1C, using a primer containing R2 at its 3' end.
 CC The invention also encompasses primers for the method of the invention,
 CC and methods for the detection of a nucleic acid sequence in a sample
 CC using a labeled probe containing a sequence complementary to the loop
 CC region of the target sequence. The method of the invention provides
 CC an efficient and highly specific method for isothermal amplification
 CC of a target nucleic acid sequence using a simple reagent mixture.
 CC The present sequence represents a prostate specific antigen (PSA)
 CC gene fragment used as a template for the method of the invention.
 XX

Sequence 517 BP; 94 A; 163 C; 151 G; 109 T; 0 other;
 Query Match 100.0%; Score 27; DB 21; Length 517;
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Gaps 0;
 Matches 27; Conservative 0; Indels 0;

OY 1 GTTCTGTGCACCCCACTGGTCTC 27
 ||||||||||||||||||||
 DB 181 GTTCTGTGCACCCCACTGGTCTC 207

RESULT 7
 ID AAH41845 standard; DNA; 517 BP.
 XX
 AC AAH41845;
 XX
 DT 30-AUG-2001 (first entry)
 XX
 DE Prostate specific antigen related nucleotide sequence.
 XX
 KM Prostate specific antigen; nucleic acid synthesis; detection; ds.
 XX
 OS Unidentified.
 XX
 PN WO200134790-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 28-MAR-2000; 2000WO-JP01919.
 XX
 PR 08-NOV-1999; 99WO-JP06213.
 XX
 PA (EIKEN) EIKEN KAGAKU KK.
 XX
 PI Notomi T, Hase T;
 XX
 DR WPI; 2001-343603/36.
 XX
 PT Synthesizing nucleic acids -
 XX
 PS Example 8; Fig 17; 96pp; Japanese.
 XX
 CC The present invention describes a new method for synthesizing nucleic
 CC acids comprising: (a) preparing a nucleic acid, with an F2c region, able
 CC to form a loop by annealing the F1 region of the 3' end to the F1c
 CC region on the same chain; (b) synthesis of a complementary chain using
 CC the 3' end of F1 as the starting point; (c) replacing the complementary
 CC chain by annealing an oligonucleotide containing F2' (complementary to
 CC F2c) at its 3' end and using it as a starting point for complementary
 CC chain synthesis by a polymerase; and (d) replacing the chain synthesised
 CC in step c by annealing a polynucleotide containing a region
 CC complementary to a part of the chain and using its 3' end as the
 CC starting point. Also described are: (1) a kit for synthesizing nucleic
 CC acids; and (2) a kit for detecting target base sequences. The present

CC sequence represents a prostate specific antigen related nucleotide
 CC sequence, which is used in an example from the present invention.
 XX

Sequence 517 BP; 94 A; 163 C; 151 G; 109 T; 0 other;
 Query Match 100.0%; Score 27; DB 22; Length 517;
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Gaps 0;
 Matches 27; Conservative 0; Indels 0;

OY 1 GTTCTGTGCACCCCACTGGTCTC 27
 ||||||||||||||||||||
 DB 181 GTTCTGTGCACCCCACTGGTCTC 207

RESULT 8
 ID AAX08947 standard; cDNA; 711 BP.
 XX

AC AAX08947;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE Human prostate specific antigen (PSA) gene.
 XX
 KM Human kallikrein 2; hk2; breast cancer; diagnosis; detection;
 KW treatment; monitoring; prostate specific antigen; PSA; ds.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT CDS 1..711
 FT /tag= a
 FT /label= Prostate-specific_antigen

PN WO9859073-A1.
 XX
 PD 30-DEC-1998.
 XX
 PF 19-JUN-1998; 98WO-US12840.
 XX
 PR 20-JUN-1997; 97US-0050963.
 XX
 PA (KLEE/) KLEE G. G.
 PA (MAYO-) MAYO FOUNDATION.
 PA (TIND/) TINDALL D J.
 PA (YOUN/) YOUNG C Y F.
 XX
 PI Klee GG, Tindall DJ, Young CYF;
 XX
 DR WPI; 1999-105632/09.
 DR P-PSDB; AAW96187.
 XX
 PT Use of human kallikrein 2 - as a marker for developing products for
 XX the diagnosis, prognosis, monitoring and treatment of breast cancer
 XX
 PS Disclosure: Page 34-35; 67pp; English.
 XX
 CC Human kallikrein 2 (hk2) is expressed at elevated levels relative to
 CC the prostate cancer antigen, prostate specific antigen (PSA) by
 CC breast cancer cells when stimulated by androgens. Detecting levels
 CC of hk2 may provide a simple diagnostic tool for detecting or
 CC determining breast cancer. Detecting hk2 is achieved by producing
 CC an hk2 DNA from hk2 RNA by reverse transcription. The hk2 DNA
 CC obtained is then amplified by PCR and detected using probes.
 CC Determination of breast cancer may also be determined by exposing
 CC the hk2 polypeptide to an agent which binds to it and then detecting
 CC the binary complex formed. The amount of complex formed correlates
 CC directly to the presence of breast cancer in the human individual.
 CC The methods can be used in the diagnosis, treatment and/or
 CC monitoring of the progression or remission of breast cancer and/or
 CC monitoring hk2 levels.
 XX
 XX Sequence 711 BP; 148 A; 208 C; 206 G; 149 T; 0 other;

Query Match 100.0%; Score 27; DB 20; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27
DB 85 GTTCTGTCACCCCGAGTGGTCCTC 111

RESULT 9
ABK86205
ID ABK86205 standard; cDNA; 744 BP.

AC ABK86205;

DT 24-SEP-2002 (first entry)

DE cDNA encoding human prostate specific antigen (PSA) variant.

KW Human; prostate specific antigen; PSA; cytostatic; antiviral;
KW Immunostimulant; cell-mediated immune response; tumour; breast cancer;
KW Virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
KW Lymphoma; leukemia; hepatitis; lentivirus; herpesvirus;
KW human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.

OS Homo sapiens.

PH Location/Qualifiers

FT key

7..744

FT CDS /tag- a
FT /product- "Prostate specific antigen (PSA) variant
with signal sequence deleted"

PN MO200240059-A2.

PD 23-MAY-2002.

PF 01-NOV-2001; 2001MO-US45626.

PR 01-NOV-2000; 2000US-0704232.

PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.

PA (MNC/) MINCHEFF M S.

PA (LOUK/) LOUKINOV D I.

PA (ZOUB/) ZOUBAK S.

PI Mincheff MS, Loukinov DI, Zoubak S;

DR WPI: 2002-527524/56.

DR P-PSDB: AAU98921.

PT Inducing a cell-mediated immune response against a target antigen,

PT reducing undesired cells and stimulating presentation of an antigen by

PT a cell, comprises administering a polynucleotide encoding a variant of

PT an antigen -

PS Disclosure: Page 121-122; 146pp; English.

CC The invention relates to a method of inducing a cell-mediated immune
CC response against a cell comprising a target antigen (I) in a subject,
CC treating a subject having undesired cells, for example tumour cells,
CC or virally infected cells (C), reducing the number of (C) in a subject,
CC and stimulating presentation of (I) by a cell. This is done by
CC administering a polynucleotide (II) encoding a variant of (I), so that
CC (II) expressed in a cell and cell-mediated immune response is induced.
CC The method can be used to treat prostate cancer, breast cancer,
CC colorectal cancer and pancreatic cancer, as well as lymphomas and
CC leukemias. The method is also useful in treating chronic viral
CC infections such as those caused by hepatitis, lentiviruses and
CC (including human immunodeficiency virus (HIV)), herpesviruses and the
CC flaviviruses and pestiviruses. The present sequence represents the coding
CC sequence of human prostate specific antigen (PSA) variant which

CC has the signal sequence deleted, used as a target antigen in the method
CC of the invention.

SQ Sequence 744 BP; 153 A; 222 C; 213 G; 156 T; 0 other;

Query Match 100.0%; Score 27; DB 24; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27
DB 115 GTTCTGTCACCCCGAGTGGTCCTC 141

RESULT 10
ABV25078
ID ABV25078 standard; cDNA; 841 BP.

AC ABV25078;

DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 25069.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001MO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI: 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 4874; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 841 BP; 144 A; 262 C; 262 G; 173 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 841;


```
XX 07-OCT-1997.
PD 29-OCT-1992: 92US-0973322.
XX 15-DEC-1994: 94US-0358782.
XX 29-OCT-1992: 92US-0973322.
PR 23-AUG-1994: 94US-0294611.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
PI Croce C, Fischer R, Gomella L, Moreno JG, Mulholland SG;
XX MPI; 1997-502328/46.
XX
XX Oligonucleotide primers specific for prostate specific antigen -
PT used for the diagnosis of prostate cancer micro-metastasis
XX
XX Example 7; Fig 2; 18pp; English.
XX
CC This DNA sequence comprises a 992-bp human prostate specific
CC antigen (PSA) cDNA PCR fragment. New oligonucleotide primers
CC (AA971044-53) are designed to amplify the PSA gene but not the human
CC glandular kallikrein gene, which has 75-85% homology to the PSA
CC gene. The primers can be used for diagnosis of prostate cancer
CC micrometastasis. A claimed diagnostic kit for detecting prostate
CC cancer comprises a pair of primers, where one of the primers is
CC selected from those given in AA971044-53, and a means for visualising
CC amplified DNA (ethidium bromide stain, 32p or biotin). The
CC invention also includes a method of detecting cells which express
CC prostate specific sequences by detecting the presence of
CC nucleic acids specific for prostate cancer or a signal specific for
CC prostate cancer.
XX
SQ Sequence 992 BP: 210 A; 291 C; 272 G; 217 T; 2 other:
XX
Query Match 100.0%; Score 27; DB 18; Length 992;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
DB 200 GTTCTGTGTCACCCCGAGTGGTCTC 226
XX
RESULT 13
AA99846
ID AA99846 standard; DNA: 992 BP.
XX
AC AA99846;
XX
XX 30-SEP-1999 (first entry)
XX
XX Prostate specific antigen PCR fragment.
XX
XX Prostate specific antigen; PSA; D1 stage prostate cancer;
XX D2 stage prostate cancer; D3 stage prostate cancer; human; diagnosis;
XX glandular kallikrein gene; micrometastasis; detection; ss.
XX
XX Homo sapiens.
XX
XX US5939258-A.
XX
XX 17-AUG-1999.
XX
XX 12-DEC-1996: 96US-0764527.
XX
XX 15-DEC-1994: 94US-0358782.
XX 29-OCT-1992: 92US-0973322.
XX 23-AUG-1994: 94US-0294611.
XX 12-DEC-1996: 96US-0764527.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
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XX
XX Croce C, Fischer R, Gomella L, Moreno JG, Mulholland SG;
XX MPI; 1999-468401/39.
XX
XX Detecting micrometastasis of prostate cancer
XX
XX Disclosure; Fig 2; 20pp; English.
XX
XX This sequence is a fragment of the human prostate specific antigen
XX (PSA). The invention relates to a method of detecting prostate cancer
XX micrometastasis in a patient having stage D1, D2, or D3 prostate cancer,
XX comprising: (1) obtaining a sample nucleic acid from a patient tissue;
XX (2) amplifying nucleic acids specific for prostate cancer or amplifying a
XX signal generated by hybridisation of a probe specific to a prostate
XX specific nucleic acid in the sample, comprising hybridisation to at least
XX 1 prostate cancer specific primer which is complementary to a prostate
XX cancer specific gene which does not hybridise to the human glandular
XX kallikrein gene; and (3) detecting the presence of the amplified nucleic
XX acids or the amplified signal where the presence of the amplified nucleic
XX acids or signal indicates micrometastasis of prostate cancer. The method
XX is useful for detecting micrometastasis of prostate cancer. The method
XX allows the detection of a low concentration of cells.
XX
SQ Sequence 992 BP: 210 A; 291 C; 272 G; 217 T; 2 other:
XX
Query Match 100.0%; Score 27; DB 20; Length 992;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
DB 200 GTTCTGTGTCACCCCGAGTGGTCTC 226
XX
RESULT 14
AAH9720
ID AAH9720 standard; cDNA: 1040 BP.
XX
AC AAH9720;
XX
XX 16-OCT-2001 (first entry)
XX
XX Human protein encoding cDNA sequence SEQ ID NO:555.
XX
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX antibacterial; endocrine; cardiant; central nervous system; viricide;
XX anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;
XX antiagregant; haemostatic; vulnery; antilucer; osteopathic; eczema;
XX dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200153455-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000: 2000WO-US35017.
XX
XX 23-DEC-1999: 99US-0471275.
XX 21-JAN-2000: 2000US-048725.
XX 25-APR-2000: 2000US-0552317.
XX
```

PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-457603/49.
 DR P-PSDB: AAM25779.
 XX
 PT Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 PS Claim 1: Page 604-605; 1217pp; English.
 XX
 CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
 CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antinaemic; antiagregant; haemostatic; vulneryary;
 CC antitumor; osteopathic; dermatologic; antiallergic; antistomatoc;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 SQ Sequence 1040 BP; 194 A; 287 C; 302 G; 257 T; 0 other;
 Query Match 100.0%; Score 27; DB 22; Length 1040;
 Best local Similarity 100.0%; Pred. No. 0.04;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTGTGTCACCCCAAGTGGTCTC 27
 DB 190 GTTCTGTGTCACCCCAAGTGGTCTC 216
 RESULT 15
 AAC03740
 ID AAC03740 standard; cDNA; 1066 BP.
 XX
 AC AAC03740;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3738.
 XX
 KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 FA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI: 2000-500381/45.
 DR

DR P-PSDB: AAG03734.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1: SEQ ID 3738; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 XX
 SQ Sequence 1066 BP; 230 A; 283 C; 310 G; 241 T; 2 other;
 Query Match 100.0%; Score 27; DB 21; Length 1066;
 Best local Similarity 100.0%; Pred. No. 0.04;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTGTGTCACCCCAAGTGGTCTC 27
 DB 199 GTTCTGTGTCACCCCAAGTGGTCTC 225

Search completed: November 19, 2002, 03:06:38
 Job time : 193.769 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 : Search time 1542.46 Seconds
(without alignments)
283.494 Million cell updates/sec

Title: US-09-829-004a-8

Perfect score: 27

Sequence: 1 gtctgtgtcaccaccagtggtctctc 27

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estclu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	316	9	AA593245
2	27	100.0	336	9	AA506459
3	27	100.0	371	9	AA503943
4	27	100.0	377	9	AA603297
5	27	100.0	397	9	AA573604
6	27	100.0	435	9	AA177005

Result No.	Score	Query Match	Length	DB ID	Description
7	27	100.0	453	9	AA533652
8	27	100.0	454	9	AT685510
9	27	100.0	465	13	BE046475
10	27	100.0	470	9	AT525128
11	27	100.0	484	9	AA603529
12	27	100.0	485	9	AA573575
13	27	100.0	495	12	BE840533
14	27	100.0	505	12	BE840441
15	27	100.0	523	9	AA639901
16	27	100.0	548	9	AA578576
17	27	100.0	552	9	BE840701
18	27	100.0	572	12	BE840537
19	27	100.0	591	12	BE679591
20	27	100.0	610	9	AT557591
21	27	100.0	638	12	BE679511
22	27	100.0	662	9	AT525089
23	27	100.0	724	12	BE964653
24	27	100.0	732	9	AT547309
25	27	100.0	737	9	AT547285
26	27	100.0	738	12	BE679168
27	27	100.0	748	12	BE973983
28	27	100.0	756	12	BE676011
29	27	100.0	770	12	BE675749
30	27	100.0	784	12	BE678386
31	27	100.0	794	12	BE675511
32	27	100.0	796	12	BE674927
33	27	100.0	797	12	BE675142
34	27	100.0	797	12	BE679394
35	27	100.0	813	12	BE681507
36	27	100.0	825	12	BE677556
37	27	100.0	828	12	BE678076
38	27	100.0	841	12	BE673766
39	27	100.0	843	12	BE675323
40	27	100.0	848	12	BE673777
41	27	100.0	849	12	BE673243
42	27	100.0	859	12	BE675660
43	27	100.0	860	12	BE675331
44	27	100.0	866	12	BE965220
45	27	100.0	868	12	BE673807

ALIGNMENTS

RESULT 1
AA593245
LOCUS
DEFINITION
AA593245
316 bp mRNA linear EST 25-SEP-1997
n07e10.s1 NCI CGAP Pr4.1 Homo sapiens CDNA clone IMAGE:1077066
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);
mRNA sequence.
ACCESSION
AA593245
VERSION
AA593245.1 GI:2409007
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 316)
NCI-CCAP http://www.nci.nlm.nih.gov/ncicgap.
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbtp/image/image.html
Insert length: 427 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 293.

FEATURES

Location/Qualifiers
1..316

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1077056"
/clone_lib="NCI_CGAP_Pt4.1"
/sex="male"
/tissue_type="prostatic intraepithelial neoplasia - high grade"
/lab_host="DH10B"

/note="Organ: prostate; Vector: PAMP10; mRNA made from prostatic intraepithelial neoplasia (high-grade), cDNA made by oligo-dt priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center"

BASE COUNT 52 a 93 c 98 g 73 t
ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.89;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 181 GTTCTGTGACACCCAGTGGTCTC 207

RESULT 2
LOCUS AA506459 336 bp. mRNA linear EST 20-AUG-1997
DEFINITION nh46a08.s1 NCI CGAP Pt5 Homo sapiens cDNA clone IMAGE:955382
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION AA506459.1 GI:2242699

VERSION AA506459
KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 336)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuangui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html

Insert Length: 442 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

Location/Qualifiers
1..336

FEATURES

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:955382"

/clone_lib="NCI_CGAP_Pt5"

/sex="male"

/tissue_type="prostate"

/lab_host="DH10B"

/note="Vector: PAMP10; mRNA made from normal prostatic

epithelial cells, cDNA made by oligo-dt priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp.

BASE COUNT

57 a 106 c 99 g 74 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.9;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 189 GTTCTGTGACACCCAGTGGTCTC 215

RESULT 3
LOCUS AA503943 371 bp. mRNA linear EST 20-AUG-1997
DEFINITION nh38d05.s1 NCI CGAP Pt5 Homo sapiens cDNA clone IMAGE:954633
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION AA503943.1 GI:2238910

VERSION AA503943
KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 371)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuangui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html

Insert Length: 454 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 365.

Location/Qualifiers
1..371

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:954633"

/clone_lib="NCI_CGAP_Pt5"

/sex="male"

/tissue_type="prostate"

/lab_host="DH10B"

/note="Vector: PAMP10; mRNA made from normal prostatic
epithelial cells, cDNA made by oligo-dt priming.
Non-directionally cloned bp. Size-selected on agarose gel,
average insert size 600 bp."

BASE COUNT 63 a 112 c 111 g 85 t

Query Match 100.0%; Score 27; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.9;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 182 GTTCTGTGACACCCAGTGGTCTC 208

RESULT 4
AA603297/c

LOCUS AA603297 377 bp mRNA linear EST 21-OCT-1997
 DEFINITION nrl2c11.s1 NCI CGAP Pr3 Homo sapiens cDNA clone IMAGE:116116
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA603297
 VERSION AA603297.1 GI:2437158
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 377)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
 Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html.
 Insert Length: 449 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 345.
 Location/Qualifiers
 1. 377
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:116116"
 /clone_lib="NCI_CGAP_Pr3"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10,
 000 microdissected cells histologically-determined to be
 fully malignant prostate cancer cells. Double-stranded
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
 applied to the cDNA with an adaptor-specific primer, and
 the resulting PCR product subcloned into PAMP10 by the
 UDG-cloning method (Life Technologies). Average insert
 size is 600 bp. NOTE: Not directionally cloned. This
 library was constructed by David Kitzman."
 BASE COUNT 90 a 130 c 97 g 60 t
 ORIGIN
 Query Match 100.0%; Score 27; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTTCTGTCACACCCAGTGGTCTC 27
 |||||||||||||||||||||
 Db 288 GTTCTGTCACACCCAGTGGTCTC 262
 RESULT 5
 LOCUS AA573604 397 bp mRNA linear EST 12-SEP-1997
 DEFINITION n142d12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:916439
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA573604
 VERSION AA573604.1 GI:2348132
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 397)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,
 Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1526 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 350.
 Location/Qualifiers
 1. 397
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:916439"
 /clone_lib="NCI_CGAP_Pr2"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10,
 000 microdissected preneoplastic cells
 histologically-determined to be prostatic intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer, and the resulting
 PCR product subcloned into PAMP10 by the UDG-cloning
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Kitzman."
 BASE COUNT 78 a 124 c 116 g 79 t
 ORIGIN
 Query Match 100.0%; Score 27; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTTCTGTCACACCCAGTGGTCTC 27
 |||||||||||||||||||||
 Db 95 GTTCTGTCACACCCAGTGGTCTC 121
 RESULT 6
 LOCUS AA177005 435 bp mRNA linear EST 14-AUG-1997
 DEFINITION nc03b02.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:302 similar
 to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA177005
 VERSION AA177005.1 GI:1758143
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.

Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 CDNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bdrip/image/image.html
 Seq primer: -40M13 fwd. from Amersham.

FEATURES

source
 Location/Qualifiers

1.435
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:302"
 /clone_lib="NCI-CGAP_Pr2"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMP10; Site-1: NotI; Site-2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 ,000 microdissected preneoplastic cells
 histologically-determined to be prostatic intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer, and the resulting
 PCR product subcloned into PAMP10 by the ude-cloning
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Kitzman."

BASE COUNT
 ORIGIN

64 a 119 c 146 g 105 t 1 others

Query Match 100.0%; Score 27; DB 9; Length 453;
 Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
 Db 155 GTTCTGTGACACCCAGTGGTCTC 181

RESULT 7 453 bp mRNA linear EST 21-AUG-1997
 AA533652
 LOCUS n72908.s1 NCI-CGAP_Pr10 Homo sapiens CDNA clone IMAGE:998078
 DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.

ACCESSION AA533652
 VERSION AA533652.1 GI:2277668
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 453)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui,
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bdrip/image/image.html

Trace considered overall poor quality
 Insert Length: 1654 Std Error: 0.00
 Seq primer: -40M13 fwd. ET from Amersham

High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source

1.453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:998078"
 /clone_lib="NCI-CGAP_Pr10"
 /sex="male"
 /tissue_type="invasive prostate tumor"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: PAMP10; mRNA made from
 invasive prostate tumor. CDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 600 bp. Library made by D. Kitzman,
 NIH."

BASE COUNT 83 a 127 c 133 g 110 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 453;
 Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
 Db 143 GTTCTGTGACACCCAGTGGTCTC 169

RESULT 8 454 bp mRNA linear EST 27-MAY-1999
 A1685510/c tu36p10.x1 NCI-CGAP_Pr28 Homo sapiens CDNA clone IMAGE:2253115.3'
 LOCUS similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.

ACCESSION A1685510
 VERSION A1685510.1 GI:4896804
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 454)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bdrip/image/image.html
 Seq primer: -40UP from Gibco.

FEATURES
 source

1.454
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253115"
 /clone_lib="NCI-CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pT7n3D-Pac (Pharmacia)
 with a modified polylinker; plasmid DNA from the
 normalized library NCI-CGAP_Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids
 955608-986759, 1101192-1101959, and 1217928-1220615).

BASE COUNT 99 a 137 c 109 g 109 t
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 454;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27
 Db 356 GTTCTGTCACCCCGAGTGGTCCTC 330

RESULT 9
 LOCUS BI046475 465 bp mRNA linear EST 14-JUN-2001
 DEFINITION MN3-FN0209-070201-010-b11 FN0209 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI046475
 VERSION BI046475.1 GI:14453097
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 465)

REFERENCE
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL sequence tags
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT 20202663

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?PL=MR3&t2=MN3-FN0209-
 070201-010-b11&t3=2001-02-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 465.
 location/Qualifiers

FEATURES
 source
 1..465
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0209"
 /dev_stage="Adult"
 /note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
 ; Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 BASE COUNT 83 a 134 c 144 g 103 t 1 others
 ORIGIN

Query Match 100.0%; Score 27; DB 13; Length 465;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27
 Db 323 GTTCTGTCACCCCGAGTGGTCCTC 349

RESULT 10
 AI525128 470 bp mRNA linear EST 09-AUG-1999

LOCUS Promena-7.F01.r bytumor Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION AI525128
 ACCESSION AI525128
 VERSION AI525128.1 GI:4439263
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 470)

Huang,G.M., Ng,W.I., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.
 and Hood,L.
 Prostate cancer expression profiling by cDNA sequencing analysis
 Genomics 59 (2), 178-186 (1999)
 99339982
 COMMENT Contact: Guyang Matthew Huang
 Leroy Hood

University of Washington
 Department of Molecular Biotechnology, Box 357730, University of
 Washington, Seattle, WA 98195
 Tel: 5106280100
 Fax: 5106280108
 Email: huangm@yahoo.com.

location/Qualifiers
 1..470
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="bytumor"

/note="Organ: Prostate; Vector: pBluescript; Directional
 cDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a fresh prostate
 tumor tissues (Urology Department, University of
 Washington)."

BASE COUNT 87 a 104 c 126 g 118 t 35 others
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 470;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27
 Db 186 GTTCTGTCACCCCGAGTGGTCCTC 212

RESULT 11
 AA603529 484 bp mRNA linear EST 08-OCT-1997
 LOCUS np1508.s1 NCI-CGAP-Pt3 Homo sapiens cDNA clone IMAGE:1116375
 DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,
 mRNA sequence.
 ACCESSION AA603529
 VERSION AA603529.1 GI:2437390
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 484)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
 Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linn.gov/bdrip/image/image.html

Insert Length: 902 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 325.
 Location/Qualifiers

FEATURES

Source

1. 484
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:116375"
 /clone_lib="NCI-CGAP_P13"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMPI0; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 /000 microdissected cells histologically-determined to be
 fully malignant prostate cancer cells. Double-stranded
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
 applied to the cDNA with an adaptor-specific primer, and
 the resulting PCR product subcloned into PAMPI0 by the
 unc-enzyming method (Life Technologies). Average insert
 size is 600 bp. NOTE: Not directionally cloned. This
 library was constructed by David Krizman."
 BASE COUNT 89 a 151 c 140 g 104 t
 ORIGIN

Query Match Best Local Similarity 100.0%; Score 27; DB 9; Length 484;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTCACCCAGTGGTCTC 27
 Db 187 GTTCTGTCACCCAGTGGTCTC 213

RESULT 12
 AA573575 485 bp mRNA linear EST 12-SEP-1997
 LOCUS n141f10.s1 NCI-CGAP_P12 Homo sapiens cDNA clone IMAGE:916363
 DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PROCURSOR (HUMAN);
 mRNA sequence.
 AA573575
 VERSION AA573575.1 GI:2348103
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL
 COMMENT Unpublished (1997)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: cgapbs-rc@mail.nih.gov
 TITLE: c9apbs-rc@mail.nih.gov
 MICHIEL EMMEBT-BUCK, M.D.; Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linn.gov/bdrip/image/image.html

Trace considered overall poor quality
 Insert Length: 1535 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

Source

1. 485
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:916363"
 /clone_lib="NCI-CGAP_P12"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: PAMPI0; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 /000 microdissected preneoplastic cells
 histologically-determined to be prostate intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer, and the resulting
 PCR product subcloned into PAMPI0 by the unc-enzyming
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Krizman."
 BASE COUNT 97 a 144 c 142 g 102 t
 ORIGIN

Query Match Best Local Similarity 100.0%; Score 27; DB 9; Length 485;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTCACCCAGTGGTCTC 27
 Db 85 GTTCTGTCACCCAGTGGTCTC 111

RESULT 13
 BE840533 495 bp mRNA linear EST 22-SEP-2000
 LOCUS RCI-FN0188-260700-022-f06 FN0188.Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE840533
 ACCESSION BE840533
 VERSION BE840533.1 GI:10272911
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Dias Neto E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, M.J., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotton sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL
 MEDLINE
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This asimpson@ludwig.org.br
 Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st2-RCI-FN0188-260>
 700-022-106653-2000-07-26&t4=1)
 Seq primer: puc 12 forward
 High quality sequence stop: 495.
 Location/Qualifiers

1. 495
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0188"


```

/dev_stage="Adult"
/note="Organ: prostate,normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      125 a      161 c      131 g      77 t      1 others
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTGTGCACCCCACTGGTCTC 27
Db      307 GTTCTGTGCACCCCACTGGTCTC 281

RESULT 14
LOCUS      BE840441/c      505 bp      mRNA      linear      EST 22-SEP-2000
DEFINITION R01-FN0188-210700-021-a02 FN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE840441
VERSION      BE840441.1 GI:10272819
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 505)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=RC1-FN0188-210
700-021-a02&ts=2000-07-21&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 505.
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location/Qualifiers
1..505
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/db_xref="taxon:9606"
/clone_id="FN0188"
/dev_stage="Adult"
/note="Organ: prostate,normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      127 a      164 c      136 g      78 t
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 505;

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Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTGTGCACCCCACTGGTCTC 27
Db      304 GTTCTGTGCACCCCACTGGTCTC 278

RESULT 15
LOCUS      AA639901      523 bp      mRNA      linear      EST 23-OCT-1997
DEFINITION np08103.s1 NCI-CGAP_P3 Homo sapiens cDNA clone IMAGE:1115741
similar to gb:M1895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);.
mRNA sequence.
ACCESSION  AA639901 GI:2563680
VERSION      AA639901.1 GI:2563680
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 523)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrr/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 367.
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location/Qualifiers
1..523
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/db_xref="taxon:9606"
/clone_id="IMAGE:1115741"
/clone_id="NCI-CGAP_P3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: PAMPI0; Site_1: NotI; Site_2: EcoRI; 1st
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DNase-treated, total cellular RNA obtained from 5,000-10,
000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into PAMPI0 by the
UDC-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
BASE COUNT      100 a      160 c      152 g      111 t
ORIGIN
Query Match      100.0%; Score 27; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTGTGCACCCCACTGGTCTC 27
Db      187 GTTCTGTGCACCCCACTGGTCTC 213

Search completed: November 19, 2002, 05:17:31
Job time : 1545.46 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 52.9615 seconds
(without alignments)
156.345 Million cell updates/sec

Title: US-09-829-004a-8

Perfect score: 27
Sequence: 1 gtctctgtgaccaccagtggtctc 27

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database:

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4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/6C_COMB.seq: *
6: /cgn2_6/prodata/2/ina/6D_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	711	4	US-09-100-264-4
3	27	100.0	992	1	US-08-358-782D-13
4	27	100.0	992	2	US-08-764-527A-13
5	27	100.0	1350	4	US-09-605-785-616
6	27	100.0	1462	1	US-08-358-782D-14
7	27	100.0	1462	1	US-08-764-527A-14
8	27	100.0	1729	2	US-08-844-024-1
9	27	100.0	1729	2	US-08-718-547-1
10	27	100.0	7130	4	US-09-056-105-31
11	23.8	88.1	711	3	US-08-622-046B-2
12	23.8	88.1	711	3	US-08-622-046B-13
13	23.8	88.1	711	4	US-09-100-264-2
14	23.8	88.1	760	3	US-08-768-859A-7
15	23.8	88.1	760	3	US-08-767-820A-7
16	23.8	88.1	760	5	PCT-US95-06157-7
17	23.8	88.1	766	3	US-08-768-859A-9
18	23.8	88.1	766	3	US-08-767-820A-9
19	23.8	88.1	766	3	US-08-622-046B-6
20	23.8	88.1	766	3	US-08-622-046B-17
21	23.8	88.1	766	4	US-09-100-264-6
22	23.8	88.1	766	4	PCT-US95-06157-9
23	23.8	88.1	822	4	US-09-100-264-8
24	23.8	88.1	832	3	US-08-768-859A-5
25	23.8	88.1	832	3	US-08-768-859A-20
26	23.8	88.1	832	3	US-08-767-820A-5
27	23.8	88.1	832	3	US-08-767-820A-20

28	23.8	88.1	832	3	US-08-622-046B-4	Sequence 4, Appl
29	23.8	88.1	832	5	US-08-622-046B-15	Sequence 15, Appl
30	23.8	88.1	832	5	PCT-US95-06157-5	Sequence 5, Appl
31	23.8	88.1	1341	4	US-08-983-075D-6	Sequence 6, Appl
32	23.8	88.1	1358	4	US-08-983-075D-8	Sequence 8, Appl
33	21	77.8	21	4	US-09-493-491-11	Sequence 11, Appl
34	21	77.8	21	4	US-09-493-491-24	Sequence 24, Appl
35	20.6	76.3	1364	4	US-09-280-116-20	Sequence 20, Appl
36	19.6	72.6	45	4	US-09-605-785-790	Sequence 790, App
37	19.6	72.6	216	4	US-09-280-116-6	Sequence 6, Appl
38	19.6	72.6	234	4	US-09-605-785-328	Sequence 328, App
39	19.6	72.6	234	4	US-09-439-313-328	Sequence 328, App
40	19.6	72.6	234	4	US-09-352-616A-328	Sequence 328, App
41	19.6	72.6	234	4	US-09-232-119A-328	Sequence 328, App
42	19.6	72.6	700	4	US-09-280-116-68	Sequence 68, Appl
43	19.6	72.6	785	4	US-09-605-785-524	Sequence 524, App
44	19.6	72.6	765	4	US-09-439-313-524	Sequence 524, App
45	19.6	72.6	871	1	US-08-744-026-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-931-981A-1
Sequence 1, Application US/08931981A
Patent No. 5817798
GENERAL INFORMATION:
APPLICANT: G. Gundling
TITLE OF INVENTION: RAPID RNA ISOLATION PROCEDURE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,981A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 6179.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-3508
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA (PSA exons 2 and 3)
US-08-931-981A-1

Query Match 100.0%; Score 27; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
DB 120 GTTCTGTGACACCCAGTGGTCTC 146

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RESULT 2
US-09-100-264-4
; Sequence 4, Application US/09100264
; Patent No. 6235486
; GENERAL INFORMATION:
; APPLICANT: Young, Charles Y.F.
; APPLICANT: Tindall, Donald J.
; TITLE OF INVENTION: Method for detection of breast cancer
; FILE REFERENCE: 545.006051
; CURRENT APPLICATION NUMBER: US/09/100.264
; EARLIER APPLICATION NUMBER: US 60/050.963
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-100-264-4

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Pred. No. 0.0069; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
Db 85 GTTCTGTGTCACCCCGAGTGGTCTC 111

RESULT 3
US-08-358-782D-13
; Sequence 13, Application US/08358782D
; Patent No. 5674682
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,782D
; FILING DATE: 15-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: TJU-1327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ANTI-SENSE: NO
US-08-358-782D-13

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Best Local Similarity 100.0%; Score 27; DB 1; Length 992;
Pred. No. 0.0071; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
Db 200 GTTCTGTGTCACCCCGAGTGGTCTC 226

RESULT 4
US-08-764-527A-13
; Sequence 13, Application US/08764527A
; Patent No. 5939258
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,527A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,782
; FILING DATE: 15-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: TJU-1327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-764-527A-13

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 992;
Pred. No. 0.0071; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
Db 200 GTTCTGTGTCACCCCGAGTGGTCTC 226

RESULT 5
US-09-605-785-616
; Sequence 616, Application US/09605785
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Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 616
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-616

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Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 778 GTTCTGTGCACCCCGAGTGGTCCTC 804

RESULT 6
US-08-358-782D-14
Sequence 14, Application US/08358782D
Patent No. 5674682
GENERAL INFORMATION:
APPLICANT: Cioce, Carlo
APPLICANT: Gomella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
City: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-14

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Best Local Similarity 100.0%; Pred. No.: 0.0073;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGCACCCCGAGTGGTCCTC 27
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Db 181 GTTCTGTGCACCCCGAGTGGTCCTC 207

RESULT 7
US-08-764-527A-14
Sequence 14, Application US/08764527A
Patent No. 5938258
GENERAL INFORMATION:
APPLICANT: Cioce, Carlo
APPLICANT: Gomella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
TITLE OF INVENTION: Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
City: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-14

Query Match 100.0%; Score 27; DB 2; Length 1462;
Best Local Similarity 100.0%; Pred. No. 0.0073;

Tue Nov 19 15:43:53 2002

us-09-829-004a-8.rnl

Page 4

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGTCACACCCCACTGGTCTC 27
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Db 181 GTCTGTCACACCCCACTGGTCTC 207

RESULT 8
US-08-844-024-1
; Sequence 1, Application US/08844024
; Patent No. 5840494
; GENERAL INFORMATION:
; APPLICANT: Katz, Aaron E., et al.
; TITLE OF INVENTION: A Method For Molecular Staging Of
; TITLE OF INVENTION: Prostate Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,024
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,391
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43677/JPM/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..1088
US-08-844-024-1

Query Match 100.0%; Score 27; DB 2; Length 1729;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGTCACACCCCACTGGTCTC 27
|||||
Db 462 GTCTGTCACACCCCACTGGTCTC 488

RESULT 9
US-08-718-547-1
; Sequence 1, Application US/08718547
; Patent No. 5976794
; GENERAL INFORMATION:
; APPLICANT: Katz, Aaron E.; Buttyan, Ralph; Rafo, Anthony;
; APPLICANT: Olsson, Carl A.

; TITLE OF INVENTION: A Method For Molecular Staging Of
; TITLE OF INVENTION: Prostate Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,547
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43677-A-PCT/JPM/MJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..1088
US-08-718-547-1

Query Match 100.0%; Score 27; DB 2; Length 1729;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGTCACACCCCACTGGTCTC 27
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Db 462 GTCTGTCACACCCCACTGGTCTC 488

RESULT 10
US-09-056-105-31
; Sequence 31, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 7130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-31

Query Match 100.0%; Score 27; DB 4; Length 7130;

Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
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Db 2069 GTTCTGTGACACCCAGTGGTCTC 2095

RESULT 11

US-08-622-046B-2
; Sequence 2, Application US/08622046B
; Patent No. 6103237
; GENERAL INFORMATION:
; APPLICANT: Saedi, Mohammed S.
; TITLE OF INVENTION: Stable Variant HK2 Polypeptide
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-MARCH-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 476.001US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-373-6903
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-622-046B-2

Query Match 88.1%; Score 23.8; DB 3; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
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Db 85 GTCTGTGACACCCAGTGGTCTC 111

RESULT 12

US-08-622-046B-13
; Sequence 13, Application US/08622046B
; Patent No. 6103237
; GENERAL INFORMATION:
; APPLICANT: Saedi, Mohammed S.
; APPLICANT: Mikolajczyk, Stephen D.
; TITLE OF INVENTION: Stable Variant HK2 Polypeptide
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/622,046B

FILING DATE: 26-MARCH-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 476.001US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-373-6903

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-622-046B-13

Query Match 88.1%; Score 23.8; DB 3; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
|||
Db 85 GTCTGTGACACCCAGTGGTCTC 111

RESULT 13

US-09-100-264-2
; Sequence 2, Application US/09100264
; Patent No. 6235486
; GENERAL INFORMATION:
; APPLICANT: Young, Charles Y.F.
; APPLICANT: Tindall, Donald J.
; APPLICANT: Klee, George G.
; TITLE OF INVENTION: Method for detection of breast cancer
; FILE REFERENCE: 545.006US1
; CURRENT APPLICATION NUMBER: US/09/100,264
; CURRENT FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 60/050,963
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-100-264-2

Query Match 88.1%; Score 23.8; DB 4; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACACCCAGTGGTCTC 27
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Db 85 GTCTGTGACACCCAGTGGTCTC 111

RESULT 14

US-08-768-859A-7
; Sequence 7, Application US/08768859A
; Patent No. 6013471
; GENERAL INFORMATION:
; APPLICANT: Tindall, Donald J.
; APPLICANT: Young, Charles Y.F.

Tue Nov 19 15:43:53 2002

us-09-829-004a-8.rn1

Page 6

APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,859A
FILING DATE: 17-DECEMBER-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 545.002US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..720
US-08-768-859A-7

Query Match 88.1%; Score 23.8; DB 3; Length 760;
Best Local Similarity 92.6%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCTGTGTCACCCCGAGTGGTCTC 27
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DB 94 GTCTGTGTCACCCCGAGTGGTCTC 120

RESULT 15
US-08-767-820A-7
Sequence 7, Application US/08767820A
Patent No. 6093796
GENERAL INFORMATION:
APPLICANT: Tindall, Donald J.
APPLICANT: Young, Charles Y.F.
APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,820A
FILING DATE: 17-DECEMBER-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 545.002US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..720
US-08-767-820A-7

Query Match 88.1%; Score 23.8; DB 3; Length 760;
Best Local Similarity 92.6%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCTGTGTCACCCCGAGTGGTCTC 27
|||
DB 94 GTCTGTGTCACCCCGAGTGGTCTC 120

Search completed: November 19, 2002, 05:20:21
Job time : 53.9615 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:04:51 ; Search time 91.3846 Seconds
(without alignments)
111.898 Million cell updates/sec

Title: US-09-829-004A-8

Perfect score: 27
Sequence: 1 gttctgtgtacacccagtggtcttc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	27	100.0	27	10	US-09-829-004A-8
2	27	100.0	1350	10	US-09-759-143-616
3	27	100.0	1350	10	US-09-780-669-616
4	27	100.0	1350	10	US-09-822-827-616
5	27	100.0	1729	10	US-09-969-708-598
6	27	100.0	1758	10	US-09-822-827-977
7	27	100.0	2406	10	US-09-822-827-980
8	27	100.0	3423	10	US-09-755-100-5
9	27	100.0	3846	10	US-09-755-100-3
10	27	100.0	4861	10	US-09-755-100-1
11	27	100.0	4661	10	US-09-755-100-2
12	23.8	88.1	1678	10	US-09-925-300-153
13	21.2	78.5	861	10	US-09-925-297-286
14	21.2	78.5	871	10	US-09-962-833-101
15	21.2	78.5	871	10	US-09-880-107-2307
16	19.8	73.3	316	10	US-09-925-300-814
17	19.6	72.6	45	10	US-09-759-143-790
18	19.6	72.6	45	10	US-09-780-669-790
19	19.6	72.6	45	10	US-09-822-827-790

20	19.6	72.6	234	10	US-09-759-143-328	Sequence 328, App
21	19.6	72.6	234	10	US-09-780-669-328	Sequence 328, App
22	19.6	72.6	234	10	US-09-822-827-328	Sequence 328, App
23	19.6	72.6	765	10	US-09-759-143-524	Sequence 524, App
24	19.6	72.6	765	10	US-09-780-669-524	Sequence 524, App
25	19.6	72.6	765	10	US-09-822-827-524	Sequence 524, App
26	19.6	72.6	871	10	US-09-956-999-7	Sequence 7, Appli
27	19.6	72.6	1119	10	US-09-759-143-177	Sequence 177, App
28	19.6	72.6	1119	10	US-09-780-669-177	Sequence 177, App
29	19.6	72.6	1119	10	US-09-030-606-177	Sequence 177, App
30	19.6	72.6	1119	10	US-09-822-827-177	Sequence 177, App
31	19.6	72.6	1119	10	US-09-115-453-177	Sequence 175, App
32	19.6	72.6	1167	10	US-09-759-143-175	Sequence 175, App
33	19.6	72.6	1167	10	US-09-780-669-175	Sequence 175, App
34	19.6	72.6	1167	10	US-09-030-606-175	Sequence 175, App
35	19.6	72.6	1167	10	US-09-822-827-175	Sequence 175, App
36	19.6	72.6	1167	10	US-09-115-453-175	Sequence 175, App
37	19.6	72.6	1214	10	US-09-759-143-225	Sequence 225, App
38	19.6	72.6	1214	10	US-09-780-669-225	Sequence 225, App
39	19.6	72.6	1214	10	US-09-822-827-225	Sequence 225, App
40	19.6	72.6	1214	10	US-09-115-453-225	Sequence 225, App
41	19.6	72.6	1215	10	US-09-759-143-326	Sequence 326, App
42	19.6	72.6	1215	10	US-09-780-669-326	Sequence 326, App
43	19.6	72.6	1215	10	US-09-822-827-326	Sequence 326, App
44	19.6	72.6	1248	10	US-09-759-143-171	Sequence 171, App
45	19.6	72.6	1248	10	US-09-780-669-171	Sequence 171, App

ALIGNMENTS

RESULT 1
US-09-829-004A-8
Sequence 8, Application US/09829004A
Patent No. US20020132976A1
GENERAL INFORMATION:
APPLICANT: Chong, Pele
APPLICANT: Pedyczak, Artur
APPLICANT: Sia, Charles Dwo Yuan
TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Antigen (P
FILE REFERENCE: 11014-24
CURRENT APPLICATION NUMBER: US/09/829, 004A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/195,456
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CLP314
US-09-829-004A-8

Query Match 100.0%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGAGTCTTC 27
DB 1 GTTCTGTGACCCCGAGTGAGTCTTC 27

RESULT 2
US-09-759-143-616
Sequence 616, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

```

: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolck, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C23
: CURRENT APPLICATION NUMBER: US/09/759,143
: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-759-143-616

Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCAGTGGTCTC 27
Db 778 GTTCTGTGCACCCAGTGGTCTC 804

RESULT 3
: Sequence 616, Application US/09780669
: Patent No. US20020051977A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolck, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780,669
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-780-669-616
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Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCAGTGGTCTC 27
Db 778 GTTCTGTGCACCCAGTGGTCTC 804

RESULT 4
: Sequence 616, Application US/09822827
: Patent No. US20020081680A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822,827
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-822-827-616

Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCAGTGGTCTC 27
Db 778 GTTCTGTGCACCCAGTGGTCTC 804

RESULT 5
: Sequence 398, Application US/09969708
: Patent No. US20020102532A1
: GENERAL INFORMATION:
: APPLICANT: Augustus, Meena
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
: FILE REFERENCE: 689290-70
: CURRENT APPLICATION NUMBER: US/09/969,708
: CURRENT FILING DATE: 2001-10-03
: PRIOR APPLICATION NUMBER: US/60/237,606
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,608
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,425
: PRIOR FILING DATE: 2000-10-03
: NUMBER OF SEQ ID NOS: 658
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 598
: LENGTH: 1729
: TYPE: DNA
: ORGANISM: Homosapiens
: US-09-969-708-598

Query Match      100.0%; Score 27; DB 10; Length 1729;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCAGTGGTCTC 27
Db 462 GTTCTGTGCACCCAGTGGTCTC 488

RESULT 6
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US-09-822-827-977
; Sequence 977, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 977
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-977

Query Match          100.0%; Score 27; DB 10; Length 1758;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCTGTGCACCCCCAGTGGGTCTC 27
Db 1186 GTCTGTGCACCCCCAGTGGGTCTC 1212

RESULT 7
US-09-822-827-980
; Sequence 980, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 980
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-980

Query Match          100.0%; Score 27; DB 10; Length 2406;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCTGTGCACCCCCAGTGGGTCTC 27
Db 778 GTCTGTGCACCCCCAGTGGGTCTC 804

RESULT 8
US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match          100.0%; Score 27; DB 10; Length 3423;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCTGTGCACCCCCAGTGGGTCTC 27
Db 1658 GTCTGTGCACCCCCAGTGGGTCTC 1684

RESULT 9
US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

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Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCTGTGCACCCCCAGTGGGTCTC 27
Db 2081 GTCTGTGCACCCCCAGTGGGTCTC 2107

RESULT 10
US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match          100.0%; Score 27; DB 10; Length 4661;
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Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27
Db 2896 GTTCGTGTCACCCCGAGTGGTCTC 2922

RESULT 11

US-09-755-100-2
; Sequence 2, Application US/09755100
; Patent No. US2002009189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2/86-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-2

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 4661;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27
Db 2896 GTTCGTGTCACCCCGAGTGGTCTC 2922

RESULT 12

US-09-925-300-153
; Sequence 153, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 153
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1663)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-153

Query Match
Best Local Similarity 92.6%; Score 23.8; DB 10; Length 1678;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27

Db 345 GTTCGTGTCACCCCGAGTGGTCTC 371

RESULT 13

US-09-925-297-286
; Sequence 286, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P105
; CURRENT APPLICATION NUMBER: US/09/925,297
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 286
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-297-286

Query Match
Best Local Similarity 78.5%; Score 21.2; DB 10; Length 861;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTGTGTCACCCCGAGTGGTCTC 27
Db 173 TTCTGTGTCACCCCGAGTGGTCTC 198

RESULT 14

US-09-962-832-101
; Sequence 101, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentln version 3.0
; SEQ ID NO: 101
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-101

Query Match
Best Local Similarity 78.5%; Score 21.2; DB 10; Length 871;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTGTGTCACCCCGAGTGGTCTC 27
Db 194 TTCTGTGTCACCCCGAGTGGTCTC 219

RESULT 15

US-09-880-107-2307
; Sequence 2307, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 23:02:59 : Search time 191.769 Seconds
(without alignments)
317.068 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27
Sequence: 1 aaactcagtggtgagcctcatgtt 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	27	100.0	27	AAD21363
2	27	100.0	90	AAT90073
3	27	100.0	246	AAT90074
4	27	100.0	420	ABV38513
5	27	100.0	429	ABV14332
6	27	100.0	466	ABV44545
7	27	100.0	476	ABV35419
8	27	100.0	492	ABV07463
9	27	100.0	616	ABV44248

C	10	27	100.0	632	23	ABV37397	Human prostate exp
	11	27	100.0	639	18	AAT92976	cDNA for prostate
	12	27	100.0	651	23	ABV22297	Human prostate exp
	13	27	100.0	651	23	ABV28130	Human prostate exp
	14	27	100.0	711	20	AAV08947	Human prostate exp
	15	27	100.0	744	24	ABK86205	cDNA encoding huma
	16	27	100.0	841	23	ABV25078	Human prostate exp
	17	27	100.0	990	21	AAZ47134	Human prostate-spe
	18	27	100.0	992	18	AAT91054	Human prostate spe
	19	27	100.0	992	18	AAV39846	Prostate specific
	20	27	100.0	1021	23	ABV24907	Human prostate exp
	21	27	100.0	1021	23	ABV29761	Human prostate exp
	22	27	100.0	1066	21	AAV3740	Human prostate exp
	23	27	100.0	1329	23	ABV23473	Human prostate exp
	24	27	100.0	1329	23	ABV29201	Human prostate exp
	25	27	100.0	1350	22	AAV63953	Human cDNA encodin
	26	27	100.0	1350	22	AAV38860	Human P703P/PSA fu
	27	27	100.0	1350	24	ABV23260	Human prostate exp
	28	27	100.0	1397	23	ABV23260	Prostate specific
	29	27	100.0	1445	19	AAV32497	Prostate specific
	30	27	100.0	1462	18	AAT91055	Human prostate spe
	31	27	100.0	1462	20	AAV39847	Prostate specific
	32	27	100.0	1466	19	AAV32496	Prostate specific
	33	27	100.0	1466	21	AAV11711	Human prostate-spe
	34	27	100.0	1728	17	AAT35867	Prostate-specific
	35	27	100.0	1729	16	AAT04864	Prostate-specific
	36	27	100.0	1729	24	ABV69732	Prostate cancer re
	37	27	100.0	1866	23	ABV23503	Human prostate exp
	38	27	100.0	1866	23	ABV23503	Human prostate exp
	39	27	100.0	1866	23	ABV24768	Human prostate exp
	40	27	100.0	1866	23	ABV29105	Human prostate exp
	41	27	100.0	1866	23	ABV29105	Human prostate exp
	42	27	100.0	1866	23	ABV29105	Human prostate exp
	43	27	100.0	1866	23	ABV29331	Human prostate exp
	44	27	100.0	1866	23	ABV29331	Human prostate exp
	45	27	100.0	2106	22	AAV69658	Human WT1/PSA fusi

ALIGNMENTS

RESULT 1
ID AAD21363 standard; DNA: 27 BP.

AC AAD21363;

DT 28-JAN-2002 (first entry)

XX Prostate specific antigen (PSA) derived peptide, CLP316 encoding DNA.

XX Prostate-specific antigen; PSA: immunogenic peptide; immune response;
therapy: cancer; prostate cancer; tumour metastasis; prophylaxis; ds.

XX Unidentified.

XX Key Location/Qualifiers

FT CDS

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PI Pedyczak A, Chong P, Sia CDY;
XX
XX WPI: 2001-663015/76.
DR P-PSDB: AAEL3025.
XX
XX New polypeptide, useful for treating cancers such as prostate cancer,
PT comprises prostate-specific antigen derived peptide -
XX
XX Claim 7: Page 28; 41pp: English.
XX
XX The patent discloses immunogenic peptides of prostate-specific antigen
CC (PSA) and nucleic acids encoding them. The peptides of the invention
CC are used to prepare a medicament to elicit an immune response in an
CC animal. They are used to treat cancer such as prostate cancer and
CC tumour metastasis. They are also useful for prophylaxis, for
CC preparing monoclonal or polyclonal antibodies, and in conventional
CC techniques of immunology, molecular biology, cell biology and
CC recombinant DNA technology. The present sequence is a DNA encoding
CC PSA derived peptide, CLP316.
XX
SQ Sequence 27 BP; 6 A; 6 G; 9 T; 0 other;
Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAACCTCAGTGTGTGACCTCATGTT 27
DB 1 AAACCTCAGTGTGTGACCTCATGTT 27
RESULT 2
AAT90073 standard; cDNA; 90 BP.
XX
XX AAT90073:
XX 14-APR-1998 (first entry)
XX
XX Prostate specific antigen oligo-epitope encoding DNA.
XX
XX Prostate-specific antigen; PSA; epitope; vaccine; immune response;
KM Prostatic tumour cell; human leukocyte antigen; HLA; cytotoxic;
KM T lymphocyte; cancer; ds.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH misc_difference 58..60
FT /*tag- a
FT /transl_except- (pos:58..60,aa:Cys)
XX
XX WO9735021-A2.
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04454.
XX
XX 20-MAR-1996; 96US-0618936.
XX
XX (USSH) US SEC DEPT HEALTH.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Schlom J, Tsang K, Zaremba S;
XX
XX WPI: 1997-480226/44.
XX P-PSDB: AAW27387.
XX Prostate specific antigen multiple epitope peptide - useful in
PT vaccine to produce immune response against prostate specific antigen
PT in prostatic tumour cell
XX

PS Claim 21; Page 64; 85pp; English.
XX
XX The present sequence encodes a prostate specific antigen oligo-epitope
CC peptide (PSA-OP) of the present invention. The PSA-OP comprises more
CC than 1 adjoined PSA-OP which generates a prostate specific response in
CC a portion of the human population. The PSA-OP can be used to produce
CC PSA specific cytotoxic T lymphocytes, in vivo or in vitro, which can
CC kill or prevent the establishment or growth of PSA positive tumour
CC cells, i.e. to prevent or treat prostatic cancer. The products may be
CC used to elicit a PSA specific immune response. When a recombinant virus
CC is used to elicit the response it is codministered with a carrier, a
CC biological response modifier e.g. interleukin 2, 6 or 12, interferon,
CC tumour necrosis factor, granulocyte/macrophage-colony stimulating factor
CC or cyclophosphamide and an adjuvant. PSA-OP comprises multiple PSA
CC epitopes, allowing an immune response to PSA in a population of humans
CC having more than 1 HLA class I molecule type to be generated.
XX
SQ Sequence 90 BP; 23 A; 24 C; 19 G; 24 T; 0 other;
Query Match 100.0%; Score 27; DB 18; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAACCTCAGTGTGTGACCTCATGTT 27
DB 16 AAACCTCAGTGTGTGACCTCATGTT 42
RESULT 3
AAT90074 standard; cDNA; 246 BP.
XX
XX AAT90074:
XX 14-APR-1998 (first entry)
XX
XX Prostate specific antigen oligo-epitope encoding DNA.
XX
XX Prostate specific antigen; PSA; epitope; vaccine; immune response;
KM Prostatic tumour cell; human leukocyte antigen; HLA; cytotoxic;
KM T lymphocyte; cancer; ds.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX
XX WO9735021-A2.
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04454.
XX
XX 20-MAR-1996; 96US-0618936.
XX
XX (USSH) US SEC DEPT HEALTH.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Schlom J, Tsang K, Zaremba S;
XX
XX WPI: 1997-480226/44.
XX
XX Prostate specific antigen multiple epitope peptide - useful in
PT vaccine to produce immune response against prostate specific antigen
PT in prostatic tumour cell
XX
XX Claim 23; Page 67; 85pp; English.
XX
XX The present sequence encodes a prostate specific antigen oligo-epitope
CC peptide (PSA-OP) for use in a virus vector of the present invention. The
CC PSA-OP comprises more than 1 adjoined PSA-OP which generates a prostate
CC specific response in a portion of the human population. The PSA-OP can
CC be used to produce PSA specific cytotoxic T lymphocytes, in vivo or in
CC vitro, which can kill or prevent the establishment or growth of PSA

CC positive tumour cells, i.e. to prevent or treat prostatic cancer. The
CC products may be used to elicit a PSA specific immune response. When a
CC recombinant virus is used to elicit the response it is coadministered
CC with a carrier, a biological response modifier e.g. interleukin 2, 6 or
CC 12, interferon, tumour necrosis factor, granulocyte/macrophage-colony
CC stimulating factor or cyclophosphamide and an adjuvant selected from
CC RIBI Detox, QS21, alum and incomplete Freund's adjuvant. PSA-OP
CC comprises multiple PSA epitopes, allowing an immune response to PSA in
CC a population of humans having more than 1 HLA class I molecule type to
CC be generated.

XX
SQ Sequence 246 BP; 56 A; 51 C; 57 G; 82 T; 0 other;

Query Match 100.0%; Score 27; DB 18; Length 246;

Best Local Similarity 100.0%; Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;

Db 150 AACCTCAGTGTGTGACCTCCATGTT 27
|||||

RESULT 4
ABV38513 standard; cDNA; 420 BP.

XX AC ABV38513;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 38504.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.

XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX PS WPI; 2001-662795/76.

XX Claim 1; Page 7841-7842; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 420 BP; 94 A; 127 C; 115 G; 84 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 420;

Best Local Similarity 100.0%; Pred. No. 0.0084; Mismatches 0; Indels 0; Gaps 0;

Db 362 AACCTCAGTGTGTGACCTCCATGTT 388
|||||

RESULT 5

ABV14332/C
ID ABV14332 standard; cDNA; 429 BP.

XX AC ABV14332;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 14323.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.

XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX PS WPI; 2001-662795/76.

XX Claim 1; Page 2391; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 429 BP; 95 A; 122 C; 121 G; 91 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAACCTCAGTGTGTGACCTCCATGTT 27
|||||
231 AAACCTCAGTGTGTGACCTCCATGTT 205

RESULT 6
ABV44545
ID ABV44545 standard; cDNA: 466 BP.
XX
AC ABV44545;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 44536.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 8836; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 466 BP; 98 A; 140 C; 136 G; 92 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAACCTCAGTGTGTGACCTCCATGTT 27

DB 328 AAACCTCAGTGTGTGACCTCCATGTT 354
|||||

RESULT 7
ABV35419/C
ID ABV35419 standard; cDNA: 476 BP.
XX
AC ABV35419;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 35410.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 7378; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 476 BP; 103 A; 138 C; 136 G; 99 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAACCTCAGTGTGTGACCTCCATGTT 27
|||||
286 AAACCTCAGTGTGTGACCTCCATGTT 260

RESULT 8
ABV07463/C

ID ABV07463 standard; cDNA; 492 BP.
XX
AC ABV07463:
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 7454.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 1204-1205; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 492 BP; 102 A; 141 C; 115 G; 134 T; 0 other;
XX
QY
Query Match 100.0%; Score 27; DB 23; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 245 AAACCTCAGTGTGGACCTCCATGTT 27
1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
ABV44248 standard; cDNA; 616 BP.
XX
AC ABV44248:
XX
DT 16-SEP-2002 (first entry)
XX

DE Human prostate expression marker cDNA 44239.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8788; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 616 BP; 122 A; 176 C; 186 G; 132 T; 0 other;
XX
QY
Query Match 100.0%; Score 27; DB 23; Length 616;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 252 AAACCTCAGTGTGGACCTCCATGTT 27
1 AAACCTCAGTGTGGACCTCCATGTT 27
|||||
ABV37397 standard; cDNA; 632 BP.
XX
AC ABV37397:
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 37388.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 PS Claim 1; Page 3854; 11750bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 SQ Sequence 651 BP; 164 A; 171 C; 156 G; 160 T; 0 other;
 XX
 QY Query Match 100.0%; Score 27; DB 23; Length 651;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AACCTCAGTGTGTGACCTCCATGTT 27
 ID AAV28130
 AC AAV28130;
 XX
 DE 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker CDNA 28121.
 XX
 KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 5827; 11750bp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 SQ Sequence 651 BP; 164 A; 171 C; 156 G; 160 T; 0 other;
 XX
 QY Query Match 100.0%; Score 27; DB 23; Length 651;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AACCTCAGTGTGTGACCTCCATGTT 27
 ID AAX08947
 AC AAX08947;
 XX
 DE 27-APR-1999 (first entry)
 XX
 DE Human prostate specific antigen (PSA) gene.
 XX
 KW Human kallikrein 2; hK2; breast cancer; diagnosis; detection;
 KW treatment; monitoring; prostate specific antigen; PSA; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..711
 FT /*tag= a
 FT /label= Prostate-specific-antigen
 XX
 PN WO9859073-A1.
 XX
 PD 30-DEC-1998.
 XX
 PF 19-JUN-1998; 98WO-US12840.
 XX
 PR 20-JUN-1997; 97US-0050963.
 XX
 PA (KLEE/) KLEE G. G.
 PA (MAYO-) MAYO FOUNDATION.
 PA (TIND/) TINDALL D J.
 PA (YOUN/) YOUNG C Y F.
 XX
 PI Klee GG, Tindall DJ, Young CYF;
 XX
 DR WPI; 1999-105632/09.
 DR P-PSDB; AAW96187.
 XX
 PT Use of human kallikrein 2 - as a marker for developing products for
 PT the diagnosis, prognosis, monitoring and treatment of breast cancer
 XX
 PS Disclosure; Page 34-35; 67pp; English.
 CC
 CC Human kallikrein 2 (hK2) is expressed at elevated levels relative to
 CC the prostate cancer antigen, prostate specific antigen (PSA) by
 CC breast cancer cells when stimulated by androgens. Detecting levels

CC of hK2 may provide a simple diagnostic tool for detecting or
CC determining breast cancer. Detecting hK2 is achieved by producing
CC an hK2 DNA from hK2 RNA by reverse transcription. The hK2 DNA
CC obtained is then amplified by PCR and detected using probes.
CC Determination of breast cancer may also be determined by exposing
CC the hK2 polypeptide to an agent which binds to it and then detecting
CC the binary complex formed. The amount of complex formed correlates
CC directly to the presence of breast cancer in the human individual.
CC The methods can be used in the diagnosis, treatment and/or
CC monitoring of the progression or remission of breast cancer and/or
CC monitoring hK2 levels.

SQ Sequence 711 BP; 148 A; 208 C; 206 G; 149 T; 0 other;

Query Match	100.0%;	Score 27;	DB 20;	Length 711;
Best local similarity	100.0%;	Score No	0.0003;	

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

RESULT 15

ID ABK86205 standard; cDNA; 744 BP.

AC ABK86205;

DT 24-SEP-2002 (first entry)

DE cDNA encoding human prostate specific antigen (PSA) variant.

KW Human: prostate specific antigen; PSA: cytostatic; antiviral:
KW Immunostimulant; cell-mediated immune response; tumour; breast cancer;
KW Virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
KW Lymphoma; leukemia; hepatitisvirus; lentivirus; herpesvirus;
KW Humanimmunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
XS
XS Homo sapiens.

OS Homo sapiens.

	Key	Location/Qualifiers
FH	CDS	7..744
FT		

	FT	FT	FT
/product=	"Prostate specific antigen (PSA) variant with signal sequence deleted"		

PN W0200240059-A2.

PD 23-MAY-2002

01-NOV-2001; 2001WO-US45626.

PR 01-NOV-2000; 2000US-0704232.

PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
...

PI Mincheff MS, Loukinov DI, Zoubak S;

DR WPI; 2002-527524/56.

DR P-PSDB; AAU98921.

PT Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by PT a cell, comprises administering a polynucleotide encoding a variant of PT an antigen -

PS Disclosure; Page 121-122; 146pp; English.

CC The invention relates to a method of inducing a cell-mediated immune

CC responded against a cell comprising a target antigen (I) in a subject,
CC treating a subject having undesired cells, for example tumour cells
CC or virally infected cells (C), reducing the number of (C) in a subject,
CC and stimulating presentation of (I) by a cell. This is done by
CC administering a polynucleotide (II) encoding a variant of (I), so that
CC (II) expressed in a cell and cell-mediated immune response is induced.
CC The method can be used to treat prostate cancer, breast cancer,
CC colorectal cancer and pancreatic cancer, as well as lymphomas and
CC leukemias. The method is also useful in treating chronic viral
CC infections such as those caused by hepatitisviruses, lentiviruses
CC (including human immunodeficiency virus (HIV)), herpesviruses and the
CC flaviviruses and pestiviruses. The present sequence represents the coding
CC sequence of human prostate specific antigen (PSA) variant which
CC has the signal sequence deleted, used as a target antigen in the method
CC of the invention.

Sequence 744 BP; 153 A; 222 C; 213 G; 156 T; 0 other;

Query Match	100.0%;	Score 27;	DB 24;	Length 744;
Post Local Similarity	100.0%;	Prod No	0.0093;	

Matches	27;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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```

oy      1  AAAC TTCAGTGTGTGGACCTCCATGTT 27
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Db      466 AAAC TTCAGTGTGTGGACCTCCATGTT 492

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Search completed: November 19, 2002, 03:06:38
Job time : 191.769 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 52.9615 Seconds
(without alignments)
156.345 Million cell updates/sec

Title: US-09-829-004a-9

Perfect score: 27
Sequence: 1 aaacttcagtggtgacctcattgt 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	711	4	US-09-100-264-4
2	27	100.0	992	1	US-08-358-782D-13
3	27	100.0	992	2	US-08-764-527A-13
4	27	100.0	1350	4	US-09-605-785-616
5	27	100.0	1452	1	US-08-358-782D-14
6	27	100.0	1452	2	US-08-764-527A-14
7	27	100.0	1729	2	US-08-844-024-1
8	27	100.0	1729	2	US-08-718-547-1
9	27	100.0	7130	4	US-09-056-105-31
10	27	100.0	7130	4	US-08-294-611-1
11	20	74.1	20	1	US-08-358-782D-1
12	20	74.1	20	1	US-08-596-993-1
13	20	74.1	20	1	US-08-764-527A-1
14	18.2	67.4	711	3	US-08-622-046B-2
15	18.2	67.4	711	3	US-08-622-046B-13
16	18.2	67.4	711	4	US-09-100-264-2
17	18.2	67.4	760	3	US-08-767-820A-7
18	18.2	67.4	760	3	US-08-768-859A-7
19	18.2	67.4	760	5	PCT-US95-06157-7
20	18.2	67.4	766	3	US-08-768-859A-9
21	18.2	67.4	766	3	US-08-767-820A-9
22	18.2	67.4	766	3	US-08-622-046B-6
23	18.2	67.4	766	3	US-08-622-046B-17
24	18.2	67.4	766	4	US-09-100-264-6
25	18.2	67.4	766	5	PCT-US95-06157-9
26	18.2	67.4	822	4	US-09-100-264-8
27	18.2	67.4	832	3	US-08-768-859A-5

28	18.2	67.4	832	3	US-08-768-859A-20	Sequence 20, Appl
29	18.2	67.4	832	3	US-08-767-820A-5	Sequence 5, Appl
30	18.2	67.4	832	3	US-08-767-820A-20	Sequence 20, Appl
31	18.2	67.4	832	3	US-08-622-046B-4	Sequence 4, Appl
32	18.2	67.4	832	3	US-08-622-046B-15	Sequence 15, Appl
33	18.2	67.4	832	5	PCT-US95-06157-5	Sequence 5, Appl
34	18.2	67.4	1341	4	US-08-983-075D-6	Sequence 6, Appl
35	18.2	67.4	1358	4	US-08-983-075D-8	Sequence 8, Appl
36	18.2	67.4	2417	4	US-09-605-785-334	Sequence 334, App
37	18.2	67.4	2417	4	US-09-352-616A-334	Sequence 334, App
38	18.2	67.4	2417	4	US-09-232-149A-334	Sequence 334, App
39	18.2	67.4	3674	4	US-09-605-785-698	Sequence 698, App
40	18.2	67.4	3360	1	US-08-408-420A-5	Sequence 5, Appl
41	18	66.7	3360	1	US-08-408-420A-5	Sequence 5, Appl
42	18	66.7	3360	1	US-08-714-901-5	Sequence 5, Appl
43	18	66.7	3360	3	US-08-040-741-5	Sequence 5, Appl
44	18	66.7	1548	4	US-09-099-053-1	Sequence 1, Appl
45	17.2	63.7				

ALIGNMENTS

```
RESULT 1
US-09-100-264-4 Application US/09100264
; Sequence 4, Application US/09100264
; Patent No. 6235486
; GENERAL INFORMATION:
; APPLICANT: Young, Charles Y.F.
; APPLICANT: Tindall, Donald J.
; APPLICANT: Klee, George G.
; TITLE OF INVENTION: Method for detection of breast cancer
; FILE REFERENCE: 545.006US1
; CURRENT APPLICATION NUMBER: US/09/100.264
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 60/050.963
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ. ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-100-264-4

Query Match 100.0%; Score 27; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
Db 436 AAACCTCAGTGTGGACCTCCATGTT 462

RESULT 2
US-08-358-782D-13
; Sequence 13 Application US/08358782D
; Patent No. 5674682
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-13

Query Match 100.0%; Score 27; DB 1; Length 992;
Best local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACCTCAGTGTGTGACCTCCATGTT 27
|||||
Db 551 AACCTCAGTGTGTGACCTCCATGTT 577

RESULT 3
US-08-764-527A-13
Sequence 13, Application US/08764527A
Patent No. 5938258
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gonnella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
TITLE OF INVENTION: Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-13

Query Match 100.0%; Score 27; DB 2; Length 992;
Best local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACCTCAGTGTGTGACCTCCATGTT 27
|||||
Db 551 AACCTCAGTGTGTGACCTCCATGTT 577

RESULT 4
US-09-605-785-616
Sequence 616, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jidongchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Nasir A.W.
TITLE OF INVENTION: REPAIR, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version*3.0
SEQ ID NO 616
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-616

Query Match 100.0%; Score 27; DB 4; Length 1350;
Best local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACCTCAGTGTGTGACCTCCATGTT 27
|||||
Db 1129 AACCTCAGTGTGTGACCTCCATGTT 1155

RESULT 5
US-08-358-782D-14
Sequence 14, Application US/08358782D
Patent No. 5674682
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gonnella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-14

Query Match 100.0%; Score 27; DB 1; Length 1462;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27
|||||
DB 532 AACTTCAGTGTGTGGACCTCCATGTT 558

RESULT 6
US-08-764-527A-14
Sequence 14, Application US/08764527A
Patent No. 5939258
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gemella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
TITLE OF INVENTION: Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-14

Query Match 100.0%; Score 27; DB 2; Length 1462;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27
|||||
DB 532 AACTTCAGTGTGTGGACCTCCATGTT 558

RESULT 7
US-08-844-024-1
Sequence 1, Application US/08844024
Patent No. 5840494
GENERAL INFORMATION:
APPLICANT: Katz, Aaron E., et al.
TITLE OF INVENTION: A Method For Molecular Staging Of
TITLE OF INVENTION: Prostate Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,024
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,391
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43677/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Tue Nov 19 15:43:56 2002

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Page 4

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 378..1088
US-08-844-024-1

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 1729;
Matches 27; Conservative 0; Pred. No. 0.0015; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27
DB 813 AAACCTCAGTGTGTGACCTCCATGTT 839

RESULT 8
US-08-718-547-1
Sequence 1, Application US/08718547
Patent No. 5976794

GENERAL INFORMATION:
APPLICANT: Katz, Aaron E.; Buttyan, Ralph; Raffo, Anthony;
APPLICANT: Olsson, Carl A.
TITLE OF INVENTION: A Method For Molecular Staging Of
TITLE OF INVENTION: Prostate Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,547
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43677-A-PCT/JPW/MUG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525

TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 378..1088
US-08-718-547-1

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 1729;
Matches 27; Conservative 0; Pred. No. 0.0015; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27
DB 813 AAACCTCAGTGTGTGACCTCCATGTT 839

RESULT 9
US-09-056-105-31
Sequence 31, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: RTPS, THOMAS J.
APPLICANT: MU, TONOI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 7130
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-31

Query Match
Best Local Similarity 100.0%; Score 27; DB 4; Length 7130;
Matches 27; Conservative 0; Pred. No. 0.0018; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27
DB 4200 AAACCTCAGTGTGTGACCTCCATGTT 4226

RESULT 10
US-08-294-611-1/C
Sequence 1, Application US/08294611
Patent No. 5506106
GENERAL INFORMATION:
APPLICANT: Croce et al.
TITLE OF INVENTION: Methods of Detecting
TITLE OF INVENTION: Micrometastasis Of Prostate Cancer
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
STREET: Maciewicz & No. 5506106r/s
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,611
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,322
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-0722
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic
STRANDEDNESS: Single
TOPOLOGY: Linear

ANTI-SENSE: NO
US-08-294-611-1

Query Match
Best Local Similarity 74.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGACCTC 21
Db 20 AACTTCAGTGTGTGACCTC 1

RESULT 11
US-08-358-782D-1/C
; Sequence 1, Application US/08358782D
; Patent No. 5674682
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gommella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,782D
; FILING DATE: 15-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardsell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: TJU-1327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-358-782D-1

Query Match 74.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGACCTC 21
Db 20 AACTTCAGTGTGTGACCTC 1

RESULT 12
US-08-596-993-1/C
; Sequence 1, Application US/08596993
; Patent No. 5688649
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gommella, Leonard

APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose G.
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting
; TITLE OF INVENTION: Micrometastasis of Prostate Cancer
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5688649-is
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,993
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/294,611
; FILING DATE: 23-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,322
; FILING DATE: 29-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1657
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-08-596-993-1

Query Match 74.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGACCTC 21
Db 20 AACTTCAGTGTGTGACCTC 1

RESULT 13
US-08-764-527A-1/C
; Sequence 1, Application US/08764527A
; Patent No. 5939258
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gommella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of
; TITLE OF INVENTION: Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103

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Page 6

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardsley, Robert J.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-1

Query Match
Best Local Similarity 74.1%; Score 20; DB 2; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACTCAGTGTGTGACCTC 21
DB 20 AACTCAGTGTGTGACCTC 1

RESULT 14
US-08-622-046B-2
Sequence 2, Application US/08622046B
Patent No. 6103237
GENERAL INFORMATION:
APPLICANT: Saeedi, Mohammed S.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,046B
FILING DATE: 26-MARCH-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476.001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6903
TELEFAX: 612-373-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
```

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LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-622-046B-2

Query Match
Best Local Similarity 67.4%; Score 18.2; DB 3; Length 711;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTTCAGTGTGTGACCTCATCT 26
DB 439 CTTCAGTGTGTGACCTCATCT 461

RESULT 15
US-08-622-046B-13
Sequence 13, Application US/08622046B
Patent No. 6103237
GENERAL INFORMATION:
APPLICANT: Saeedi, Mohammed S.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,046B
FILING DATE: 26-MARCH-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476.001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6903
TELEFAX: 612-373-3061
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-622-046B-13

Query Match
Best Local Similarity 67.4%; Score 18.2; DB 3; Length 711;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTTCAGTGTGTGACCTCATCT 26
DB 439 CTTCAGTGTGTGACCTCATCT 461

Search completed: November 19, 2002, 05:20:22
Job time : 53.9615 secs
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